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Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

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>	I am an examiner in Workgroup: Example: 1610
A	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
4	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Con	nments:

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104375

From: Sent: To: Subject: Slobodyansky, Elizabeth Tuesday, September 23, 2003 6:42 PM STIC-Biotech/ChemLib 09/974,973

Please search for case 09/974,973

d interference detabases

SEQ ID NOs: 2 and 19 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652 CM1 10D11 703-306-3222

mail box 10D01

Searcher:
Phone:
Location:
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Searcher Prep/Review:/
Clerical:
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TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
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Litigation:
Full text:
Patent Family:
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Questel/Orbit:	
DRLink:	
Lexis/Nexis:	67
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September 24, 2003, 15:43:18; Search time 64.4737 Seconds (without alignments) 2848.398 Million cell updates/sec
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Corynebacterium fe Corynebacterium mu Pyruvate carboxyla C glutamicum prote Corynebacterium gl Corynebacterium gl Corynebacterium gl Corynebacterium wi C. glutamicum pyru C glutamicum pyru
SUMMARIES	AAU98050 AAU98052 AAB01436 AAB01136 AAB07129 AAB05601 AAU98053 AAW3971
	2003322233
% Query Match Length DB	1157 1140 1141 1140 1140 1140 1140
% Query Match	100.0 100.0 98.3 98.2 98.2 98.2 98.2
Score	5865 5779 5779 5759 5759 5759 5759
Result No.	

18-APR-2002

Corynebacterium th	Corynebacterium gl	Bacillus subtilis	N		rn.	Staphylococcus epi	s E	Drosophila melanog	Drosophila melanog	Drosophila melanog	Drosophila melanog	Lactococcus lactis	=	Staphylococcus aur	Corynebacterium gl	Corynebacterium gl	Corynebacterium gl	Corynebacterium gl	biotin b	Anabaena biotin ca	in carboxy	()	Synechococcus biot	Synechococcus biot	A. vitis hypersens	Pseudomonas aerugi	typhi		Haemophilus influe	Streptococcus poly	Biotin-carboxyLase	E. coli cellular p	. gonorrhoeae am	hlamydia pneumo	Ctrentococolin pheli
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ALIGNMENTS

Corynebacterium feedback-resistant pyruvate carboxylase enzyme. 1..18 /note= "Specifically claimed in claim 18" 164..176 /note= "Specifically claimed in claim 18" 193..205 .205. e= "Specifically claimed in claim 18" "Specifically claimed in claim 18" /note= "Specifically claimed in claim 18" 466..478 /note= "Specifically claimed in claim 18" Feedback-resistant; pyruvate carboxylase; enzyme; aspartic acid feedback inhibition resistant. Location/Qualifiers AAU98050 standard; Protein; 1157 AA. Corynebacterium glutamicum (first entry) /note= "Sp 238..250 /note= "S 217..229 WO200231158-A2 27-AUG-2002 AAU98050; Key Region Region Region Region Region Region AAU98050 ~

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pyruvate carboxylase enzyme. The invention is useful for producing an
amino acid (e.g. L-Lyz, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro),
by culturing a host cell in a suitable media and separating the amino
coid from the medium. The vector of the invention is useful for
replacement of a wild-type pyruvate carboxylase gene, with a feedback
resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by
resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by
resistant pyruvate carboxylase gene, in a corynebacterium glutamicum, by
resistant pyruvate carboxylase gene with
selectable marker gene through homologous recombination to form a second recombinate
crecombination strain, with feedback resistant pyruvate carboxylase
gene through homologous recombination in the above steps, occurs
cretarin, where the homologous recombination in the above steps, occurs
between the host cell and the vector. The feedback-resistant pyruvate
carboxylase enzyme is resistant to feedback inhibition from aspartic
cacid. The present amino acid sequence represents the feedback-resistant
pyruvate carboxylase enzyme of the invention.
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                                                                                                                                                                                                                                     Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt RECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTY}
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Best Local Similarity 100.
Matches 1157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new mutated, feedback-resistant pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g. L.Ys, L.Thr, L.Met, L-Ile, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by replacing a genenic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 LDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 VSSPDELRKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombination strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAOLARECAENGITFIGPTPEV
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                                                                                                                                      /note= "Wild-type Asp substituted by Glu"
 "Wild-type Ala substituted by Ser"
                                                    "Wild-type His substituted by Arg"
                                                                                by Gly"
                                                                                                      /note= "Specifically claimed in claim 18"
1116
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                          "Wild-type Ala substituted by
                                                                                'note= "Wild-type Ala substituted
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                                                                                                                                                 PRIQVEHTVTEEVTEVDLVKAQMKLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG
                                                                                                                                                                                                                                                                                                                                                                PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG
                                                                                                                                                                                                  FRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRAL
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                                                    LQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN
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ADDSKERRNSLNRLLFPKFTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRT 1036
                                                                                  661 AIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKWAEEIVKSGAHILAIKDMAGLL
                                                                                                                                                                                                                                                                                                                                                                                                          FAADDQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLD
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                                                                TFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLD
                                                                                                                                ELREAMPINVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRP
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                                                                                                                                                                                              AIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The pyruvate carboxylase of Corynebacterium glutamicum can be used for producing amino acids, preferably lysine and glutamic acid in industrial fermentations and for replenishing oxaboacetate consumed for biosynthesis during growth. By incorporating the pyruvate carboxylase gene in expression vectors.levels of expression can be 2 - 20 fold higher than in Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides encoding Corynebacterium glutamicum pyruvate carboxylase useful for industrial fermentation processes comprises specific nucleotide sequence
carboxylase; expression; amino acid biosynthesis; lysine; acid; oxaloacetate; fermentation; biosynthesis.
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99.4%; Pred. No. 0;
live 5; Mismatches 2;
                                                                                                                                                                                                                                                                        Willis LB;
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 1; 51pp; English.
                                                                                                                                           98WO-US27301
                                                                                                                                                                           98WO-US27301
                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                                        PA,
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                                                                                                                                                                                                                                                                        Lessard
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LESSARD P A.
                                                                                                                                                                                                                                                                                                     2000-465746/40.
                                                                                                                                                                                                                                        WILLIS L B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                          WO200039305-A1
                                                                                                                                                                          23-DEC-1998;
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                                                                                                                                                                                                                                                                      Sinskey AJ,
                                                                                                           06-JUL-2000
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Matches 1134;
Pyruvate o
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N-PSDB; AAF32165
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                                                                                                                                                                                                              sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                       for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 VSTHISSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                   analysing
                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identify mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous.
                                                  Yokol H;
                                                                                                                                                                                                    The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                English.
                                                  Ochiai K,
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                                                Hayashi M,
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                                                            Ozaki A;
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Pred. No. 0;
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                                                Ando
                                                            Ikeda M,
                         (KYOW ) KYOWA HAKKO KOGYO KK
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 03-AUG-2000; 2000JP-0280988
                                                                                                                                                                              SEQ ID NO: 4265;
                                                Mizoguchi H,
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1133; Conservative
                                                          Senoh A,
                                                                                 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                        1140 AA;
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                                                                                             N-PSDB; AAH65730
                                              Nakagawa S,
Tateishi N,
                                                                                                                                                                              Claim 17;
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DDSKERRNSLNRLIFPRPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1020
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                                                    541 FRDAHQSILATRVRSFALKPAABAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDE
                                                                                                                                                                 PAAVIKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPS
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                                  618 LREAMPINVIIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA
                                                                                                678 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carboxylase; anaplerotic pathway; industrial fermentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum pyruvate carboxylase.
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                                               The present invention provides the protein and coding sequences of the Corynebacterium glutamicum pyruvate carboxylase protein. This is an enzyme in the anaplerotic pathway. It can be used in the replenishment oxaloacetate consumed during lysine and glutamic acid production in
                                                                                                                                                                                                                                                                                                                                                                                                                                              LDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRF
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                                                                                                                                            Length 1140;
                                                                                                                                                                    Indels
 glutamic acid production in industrial fermentations
                                                                                                                                           DB 22;
                                                                                                                                                                   2;
                                                                                                                                                                   5; Mismatches
                                                                                                                                           Score 5759;
Pred. No. 0;
                      Column 31-36; 29pp; English.
                                                                                                                                        Query Match
Best Local Similarity 99.4%;
Matches 1133; Conservative 5
                                                                                              fermentation.
                                              invention
                                                                                                                   1140 AA;
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                       Claim 1;
                                                                                                                   Sequence
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                                                                                                                                                    DDSKERRNSLNRLLFPKPTEEFLEHRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1037
                                                                                                                                       LLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1097
                                                                                                                                                                                        GVVTVTVABGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVVS 1157
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                                                   The present invention relates to novel pyruvate carboxylase proteins and polynuclectides encoding such proteins. Sequences of the invention are important anaplerotic enzymes for replenishing oxaloacetate consumed for biosynthesis during growth, or lysine and glutamic acid production in industrial fermentation. The present sequence is C. glutamicum pyruvate
AADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDA
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                                                                                                                                                                                                                                                                                                                                                                             carboxylase; anaplerotic enzyme; industrial fermentation;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                             Protein; 1140 AA
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99.48;
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Matches 1133; Conserv
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                            IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV
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The present invention relates to a new mutated, feedback-resistant pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a Corynebacterium gultamicum, by replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombination strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-1ysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the host cell and the vector. The feedback resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present amino acid sequence represents the wild-type feedback-resistant pyruvate carboxylase enzyme of the invention.
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AAU98053 standard; Protein; 1140
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Matches 1133; Conservative
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                                                               LQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN 317
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                                      PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNG
                           VSSPDELRKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCS
                                                                                                              FRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKWTCRGSDFETAVARAQRAL
                                                                                                                                                   AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADV
                                                                                                                                                                                        L'REAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA
                                                                                                                                                                                                                                                                                                   IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR
                                                                                                                                                                                                                                                                                                                                        PAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPS
                                                                                                                                                                                                                                                                                                                                                                             AADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTT
                                                                                                                                                                                                                                                     FRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEANGGATYDVAMRFLFEDPWDRLDE
                                                                                                                                                                                                                                                                                                                                                                                                       LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                           SNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF
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IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIQVEHTVIEEVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Corynebacterium glutamicum which is used in a novel method for production of lysine, threonine, homoserine, glutamate and/or arginine, variously useful as feed additives, condiments, pharmaceuticals and intermediates for fine chemicals. Increasing pyruvate carboxylase activity increases the yield of microbial production of amino acids of the asparate and/or glutamate families, e.g. about 50% more lysine, 40% more threonine and 150% more homoserine are secreted into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 VSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSSPDELRKLATEASREAERGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRAL
                                                                    Pyruvate carboxylase; amino acid production; lysine production; threonine production; homoserine production; glutamate production; arginine production; feed additive; condiment; pharmaceutical; fine chemical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes the isolation of a pyruvate carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                   ρλ
                                                                                                                                                                                                                                                                                                                                                                                                  microbial production of specific amino acids by activity or expression of pyruvate carboxylase
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                                         glutamicum pyruvate carboxylase protein.
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Pred. No. 0;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 11-15; 18pp; German.
                                                                                                                                                                                                                                                                                                                         Peters-Wendisch P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.1%;
Best Local Similarity 99.3%;
Matches 1132; Conservative
                                                                                                                                                                                                                                   98DE-1031609
                                                                                                                                                                                                                                                                 97DE-1043894
                                                                                                                                              Corynebacterium glutamicum.
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Increasing microbial increasing activity o
                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-245521/21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1140 AA;
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                                                                                                                                                                                                                                  14-JUL-1998;
                                                                                                                                                                                                                                                                 04-OCT-1997;
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180 257 317 300 377 437

AAW93971 standard; Protein; 1140 AA

RESULT 8 AAW93971 AAW93971;

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20-JUN-2001

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DDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1098 GVVTVIVAEGDEVKAGDAVAIIEAMKMEATIIASVDGKIERVVVPAATKVEGGDLIVVVS 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1097
                                                                                                                                          009
                                                                                                                                                                                                                                                                                                    720
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IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR
                                                                                                                                                                                                                  PAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPS
                               AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADV
                                                                                                                   FRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDE
                                                                                                                                                            LREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA
                                                                                                                                                                                                                                                                                        LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL
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Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                        /note= "wild-type Pro substituted by Ser"
                                                                           glutamicum protein fragment mutant P458s.
                                                                                                            organic acid synthesis; mutant; mutein.
          AAG93249 standard; Protein; 1140 AA
                                                                                                                                                                    Location/Qualifiers
                                                                                                                                   Corynebacterium glutamicum
                                                      (first entry)
                                                                                                                                                                             Misc-difference 458
                                                                                                                                                                                                             EP1108790-A2.
                                                      26-SEP-2001
                                                                                                                                              Synthetic.
AAG93249
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257 240 LORRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN 317

VSSPDELRKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCS

121

qq δ qq Q qq ŏ qq $^{\circ}$ g Qγ

377

AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADV 497

361 438 FRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRAL

PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, mesauring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a mutant protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                        mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 VSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV
                                                                                                                                                                                        Η;
                                                                                                                                                                                          Yokoi
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                                                                                                                                                                                      Ochiai K,
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                                                                                                                                                                                                                                                                                                                                                       Claim 43; Page -; 246pp + Sequence Listing; English.
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la M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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Pred. No. 0;
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Ikeda M,
                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.18;
                                                                                              2000JP-0159162.
2000JP-0280988.
                                              18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 1132; Conservative
                                                                                                                                                                                    Mizoguchi H
Senoh A,
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                                                                                                                                                                                                                                     WPI; 2001-376931/40.
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                                                                                                07-APR-2000;
03-AUG-2000;
                                                                                16-DEC-1999;
                                                                                                                                                                                  Nakagawa S,
Tateishi N,
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(AJIN) AJINOMOTO CO INC.

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DDSKERRNSINRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHSHLLQAPPADDEQGRILDYLADV 480
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                               LREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA
                                                                                                            IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR
                                                                                                                                                   LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL
                                                                                                                                                                                                                                   SNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF
                                                                                                                                                                                                                                                                                                   AADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDA
                                                                                                                                                                                                                                                                                                                                                                                               FRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDE
                                                                                                                                                                                PAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPS
                                                                                                                                                                                                                                                                         Corynebacterium; thermophilic; amino acid biosynthesis; enzyme; thermotolerant; acc8; acc8C; dtsR1; dtsR2; pfk; scr8; gluABCD;
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99JP-0311147.
2000JP-0120687.
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01-NOV-1999;
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                         E)
                                                                                                                                                  The present sequence is provided in a specification relating to genes encoding thermophilic amino acid biosynthesis system enzymes of the thermotolerant bacterium Coynebacterium thermoaminogenes. The novel proteins retain at least 30% isocitrate ligase activity after heating at 500C for 5 minutes. DNA fragments encoding the enzymes were isolated from a Corynebacterium thermoaminogenes chromosomal DNA plasmid library by PCR. The DNA may be used for developing strains of amino acid producing microorganisms.
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                                                                                               Proteins and their DNA useful for microbial production of L-amino
                                                                                                                                                                                                                                                                             Length 1139;
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                       Nakamura K,
Nakamatsu T;
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                                                                                                                                                                                                                                                                             DB 22;
                       Akiyoshi N,
                                Kurahashi O,
                                                                                                                                                                                                                                                                           ; Score 5299.5;
; Pred. No. 0;
44; Mismatches
                                                                                                                                9; Page 132-135; 215pp; Japanese.
                      Matsuzaki Y,
Kawahara Y, K
                                                                                                                                                                                                                                                                            90.4%;
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Best Local Similarity 90.9°
Matches 1036; Conservative
                      Nonaka G,
                                Matsui K,
                                                              2001-300170/31
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                                                                          N-PSDB; AAF87437
                                          Sugimoto S;
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                                                                                                                                                                                                                                                                                                                                                        SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic anino acid; purine base; pyrimidine base; nucleoside; nucleotide: lipid; saturated fatty acid; unsaturated fatty acid; disciplentate; aromatic compound; vitamin; cofactor; polyketide; disciplentation; cofactor; polyketide; disciplentationsis; Corynebacterium diphtheriae; evolutionary study.
         IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR
                               PAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFRAAQAGADAVDGASAPLSGTTSQPS
                                                              LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL
                                                                                               SNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF
                                                                                                         AADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDA
                                                                                                                                       DDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP
                                                                                                                                                                                                                                                                                                                                                   carbon metabolism and energy production;
                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum SMP protein sequence SEQ ID NO:120.
                                                                                                                                                                                                                                                                                   AAB79302 standard; Protein; 532
                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum;
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metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and cenergy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to for function, in modulating SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production is a support or the presence of its and in modulating high-energy molecule production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids,
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Pred. No. 7.5e-191;
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99DE-1042079.
99DE-1042086.
99DE-1042087.
99DE-1042088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents Bacillus subtilis pyruvate carboxylase which catalyses the carboxylation of pyruvate to form oxaloacetate. Transformation of the Bacillus subtilis pyrA gene into a bacterium belonging to the genus Escherichia results in the bacterium showing L-amino acid productivity. The invention provides a novel method for producing an L-amino acid by fermentation. The method involves cultivating the bacterium in a medium and producing and accumulating the L-amino acid in the medium. The new bacterium harbouring the gene coding for an enzyme having pyruvate carboxylase activity is useful for producing higher concentrations of L-amino acids in vitro than
                             VEFLVDEKGNHVF1EMNPR1QVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDK1KT
                                           HGAALQCRITTEDPNNGFRPDTGT1TAYRSPGGAGVRLDGAAQLGGE1TAHFDSMLVKMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New bacterium from the genus Escherichia containing a gene encoding pyruyate carboxylase useful for producing higher concentrations of
                                                                                                                                                                  PPADDEQGRILDYLADVTVNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDR 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Voroshilova
                                                                                                                                                                               oxaloacetate; Escherichia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ptitsyn LR, Altman IB,
                                                                                                                                                                                                                                                                                                             Bacillus subtilis pyruvate carboxylase enzyme A.
                                                                                                                                                                                                                                                                                                                                     Pyruvate carboxylase A; pycA; oxaloace
L-amino acid production; fermentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 17-21; 28pp; English.
                                                                                                                                                                                                                                           AAU00511 standard; Protein; 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gusyatiner MM, Kozlov YI, Pt
Iomantas YAV, Yampolskaya TA;
                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis strain 168.
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                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                   carboxylase A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS01509
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                                                                                                                                                                                                                                                                   AAU00511;
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22; Length 1148;

DB

Score 2530;

43.18;

Query Match

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1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423
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                                                                                                                                                         147
                                                                                                                                                                                   148 VTAAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRK 206
                                                                                                                                                                                                                                                                          LATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVV 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 EVAPSVSLSPELRDQICEAAVALAKNVNYINAGTVEFLV-ANNEFYFIEVNPRVQVEHTI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEEVTEVDLVKAQMRLAAGATL -- KELGLTQDK - IKTHGAALQCRITTEDPNNGFRPDTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV 442
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                                                                                                                                                      88 YLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRA
                                                                                                                                                                                                                                                                                                                                                                               185 AYERAKSEAKAAFGNDEVYVEKLIENPKHIEVQVIGDKQGNVVHLFERDCSVQRRHQKVI
                                                               28 AFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKA
                                                                                                            5 SIQKVLVANRGEIAIRIFRACTELNIRTVAVYSKEDSGSYHRYKADEAYLVGEGKKPIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              836 GGOYSNLOOQAKGVGLGDRWNEVKEMYRRVNDMFGDIVKVTPSSKVVGDMALYMVQNNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------EQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFF
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                         Gaps
                       48;
                       Indels
    Pred. No. 2.5e-179;
                       Mismatches
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533; Conservative 188;
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1008 YGMTLGEEIEVEIERGKT-LIVKLISIGEPQPDATRVVYFELNGQPREVVIKDESIKSSV 1066
                                                1079 ATAEKADSSNKGHVAAPFAGVVTVTVAE-GDEVKAGDAVAIIEAMKMEATITASVDGKIE 1137
                                                                                                                 CVHVKNGEPIQTGDLLLEI 1145
                                                                                            RVVVPAATKVEGGDLIVVV 1156
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ABB47612 standard; Protein; 1146 AA

ABB47612;

(first entry) 05-FEB-2002

Listeria monocytogenes protein #316.

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease

Listeria monocytogenes

WO200177335-A2.

18-OCT-2001

11-APR-2001; 2001WO-FR01118.

11-APR-2000; 2000FR-0004629.

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(INSP) INST PASTEUR,

Dehoux P; Cossart P; Couve E, Rusniok C, Fsihi H, Dehoux P;
Nedjari H, Glaser P, Kunst F, Cossart P
L J, Kuhn M, Ng E, Vazquez-Boland JA; Carrido-Garcia P., Tierrez-Martinez A, Amend nn E, Hain T, Berche P, Charbit A, Durant ro F, Garcia Del Portillo F, Gomez-Lopez N, os B, Wehland J, Kaerst U, Entian K, Hauf Goebel W, Kreft J, Frangeul L, Chetouani F, Dominguez-Bernal G, Garric Chakraborty T, Domann E, Perez-Diaz J, Baquero F, Maduenio E, De Pablos B, Voss H; Buchrieser C, Dussurget O, Daniels J, Rose M,

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WPI; 2002-010914/01.

for treatment ns, and Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, and prevention of Lisrelated polypeptides

Claim 6; SEQ ID No 317; 192pp; French.

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monocytogenes and related organisms, and for studying genetic problems are considered organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of E. monocytogenes and related organisms, and for blosynthesis and biodegradation, especially biosynthesis of vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome various compositions for the second proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. of L. The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in

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qq

1146 AA; Sequence

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11;
                                                                                                                                                                                                               DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621 AMPNVNIQMLIRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDA 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VREAG-KVVEAAICYTGDIDDDTRIKYTIDYYKDMAKELVAQGTHILGIKDMAGLLKPQA 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               681 VLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 QIPNVMFQMLLRGANAVGYKNYPDNVIREFVKQSAQSGVDVFRVFDSLNWIKGMEVSIDA 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAAD 920
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                                                                                                                                                 5 KKVLVANRGEIAIRVMRACTELKIKTVAIYSQEDIGSFHRYKSDEAYLVGAGKKPIDAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL
                                                                                                                                                                                                                                                                                                                    150 AAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLA
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                                                                                                                                                                                                                                                                                                                                                                                                                               209 TEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 TAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKHRD--KPVYAEPRLPKIPYGSQISPGTKQILDAKGPEGVVDWVKKQEEVLLTDTTLRD
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                                                          Gaps
                                                          30;
     Length 1146;
                                                          Indels
     DB 23;
                                                        408;
cch 42.5%; Score 2494; DB 23; 11 Similarity 45.7%; Pred. No. 1.2e-176; 525; Conservative 186; Mismatches 408;
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Query Match
Best Local 9
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                                                  Matches
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ftp.wipo.int/pub/published_pct_sequences

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella premoniae, Pseudomonas aeruginosa and Enterococcus facelis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acid sequence is also useful to screen compounds in retional drug discovery programmes. The antisense nucleic acid sequence represents an avide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
 RLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNK 1089
                                                                 1090 GHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAATKVE 1148
                                                                                     1017 ELEKGKI-LLIKLNSIGEPIADGTRVIYFELNGQPREINIQDMNVQSTVIARRKIDTTNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cellular proliferation protein #248.
                                                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                       AAU33972 standard; Protein; 1147 AA.
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2000US-207727P.
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2000US-257931P.
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                                                                                                                                     1149 GGDLIVVVS 1157
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26-MAY-2000;
23-OCT-2000;
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22-DEC-2000;
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964 LIEVPEEEQAHLDADDSKE------RRNSLNRLLFPKPTEEFLEHRRRFGNTSAL 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 RGVKTNIPFLINVMKNKKFTSGDYTIKFIEETPELFDIQPSLDRGTKTLEYIGNVTIN-- 478
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                                                                                                                                     63
                                                                                                                          30 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL
                                                                                                                                                             DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT
                                                                                                                                                                                                                  150 AAKKAGLPVL-AESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLA
                                                                                                                                                                                                                                           124 TAIKADLPVIPGTDGPIKSYELAKEFAEEAGFPLMIKATSGGGGKGMRIVREESELEDAF
                                                                                                                                                                                                                                                                                                                            269 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLV--DEKGNHVF1EMNPRIQVEHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 LREQDALAVIDITFRDAHQSLLATRVRSFALKPAAEAVAKLIPELLSVEAWGGATYDVAM
                                                                                                                                                                                                                                                                      209 TEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 GASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAVASMSGLTSQPSANSLYYALNGFPRHLRTDIEGMESLSHYWSTVRTYYSDFESDIKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         844 TGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDL
                                                                                  Gaps
                                                                                 62;
                                                      Length 1147;
                                                                                 Indels
                                                    Score 2489; DB 22;
Pred. No. 2.9e-176;
                                                                  42.48;
                           1147 AA;
                           Seguence
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                                                    Query Match
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Tilly given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(II) and (II) can have antibacterial activity and therefore can be used to produce the in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent objections lessent invention. AAH55091 to AAH55090 represent oligonuclectide sequences from the present invention. AAH55091 to in the exemplification of the present invention.
N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472,
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                                                                                                                                            DDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDR
                                                                                                                                                                                                                                   SVESVTATAEKADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:2448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. epidermidis open reading frame protein sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                         1132 VDGKIERVVVPAATKVEGGDLIVVV 1156
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                                                                                                                               KAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKS 145
                                                                                                                                               264
                                                                                                                                                                                                                                                                                                                                                                                                    |||:|| :| :|| || :| || :| || EHITTEMITGIDIVKTQILVADGESLFGDKISMPQQNEIQTLGYAAIQCRITTEDPTNDFM 361
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                                                                                                 64
                                                                                              LKQIKKLLVANRGEIAIRIFRAAAELNISTVAIYSNEDKSSLHRYKADESYLVGSDLGPA
                                                                                                                                                                                          RAVTAAKKAGLPVL-AESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDEL
                                                                                                                                                                                                                                                                         185 EDAFHRAKSEAEKSFGNSEVYIERYIDNPKHIEVQVIGDEFGNIIHLYERDCSVQRRHQK
                                                                                                                                                                                                                                                                                                                      VVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLV--DEKGNHVFIEMNPRIQV
                                                                                                                                                                                                                                                                                                                                                    VVEVAPSVGLSNKLRERICDAAIQLMENIKYVNAGTVEFLVSGDE---FFFIEVNPRVQV
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                                                                                                                                                                                                                                                       RKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INGFPNVEKRPKP-EYESTKIPKISQKKINQLFGTKQILEQHGPTGVTNWVREQEDVLIT
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                                     Gaps
                                  34;
    Length 1151;
                                    Indels
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1023 EGRETLIRLPDVRIDILJVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESYTATAE 1082 	1083 KADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVALIEAMKMEATITASVDGKIERVVV 1141 1075 KADKSNPNHIGAQMPGSVTEVKVSVGDEVQANQPLLITEAMKMETTIQAPFDGIIKQINV 1134	1142 PAATKVEGGDLIVVV 1156 : : : 1135 ANGDAIATGDLIVEI 1149	Search completed: September 24, 2003, 15:55:21 Job time : 70.4737 secs
1023 EG 1016 NG	1083 KA 1075 KA	1142 PA 1135 AN	ompleted : 70.47
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 24, 2003, 15:27:07; Search time 18.1332 Seconds (without alignments) 2699.668 Million cell updates/sec Run on:

US-09-974-973A-2 5865 Perfect score:

1 MTAITLGGLLLKGIITLVST.....RVVVPAATKVEGGDLIVVVS 1157 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 seqs, 42310858 residues Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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                                                    GENERAL INFORMATION:
APPLICANT: Sinskey, Anthony J.
APPLICANT: Lessard, Philip A.
APPLICANT: Willis, Laura B.
APPLICANT: Stephanopoulos, Gregory
IITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
FILE REFERENCE: 1533.0790000
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CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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                    Sequence 2, Application US/09220081 Patent No. 6171833
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Sinskey, Anthony J.

APPLICANT: Lessard, Philip A.

APPLICANT: Lessard, Philip A.

APPLICANT: Mills, Laura B.

APPLICANT: Stephanopoulos, Gregory

TITLE OF INVENTION: Pytuvate Carboxylase from Corynebacterium glutamicum

FILE REFERENCE: 1533.0790000

CURRENT APPLICATION NUMBER: 08/09/677,575

CURRENT FILING DATE: 2000-10-03

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.0

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ORGANISM: Corynebacterium glutamicum
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Patent No. 6403351
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APPLICANT: MAO, JEN-1
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
ITILE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
ITILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CORRESPONDENCES: 411
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          LLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1097
                                                                 GVVTVTVABEGDEVKAGDAVALIEAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVVS 1157
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                           2 FSKVLVANRGEIAIRAFRAAYELGVGTVAVYPYEDRNSQHRLKADESYQIGDIGHPVHAY
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llarity 62.2%; Pred. No. 4.6e-267;
Conservative 151; Mismatches 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               Sequence 10, Application US/08311731A Patent No. 6583266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEPHONE: 617/720-341
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MEDIUM TYPE: Floppy
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                      EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 388
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                                                                                                                                                                                                    Length 1154;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                 42.0%; Score 2465; DB 4;
llarity 45.4%; Pred. No. 2.7e-186;
Conservative 198; Mismatches 399;
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-12
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3428
                                                                                                                                                 ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                US-09-134-001C-3428
                                                                                                                  1154
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and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                         974 HLDAD ------DSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLV 1022
                                                                                                                                                                                                                         957 PVDFEAIRQELSDIQQDEVTEQDIISYVLYPKVYKQYIQTKEQFGNVSLLDTFTFLFGMR 1016
                                                                          PADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQA 973
                                                                                                                          901 EDTVINDGYKLDFPESVVSFFKGDIGQPVNGFNKKLQDVILKGQQ----PITERPGEYLE 956
1023 EGRETLIRLPDVRIPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESYTATAE
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...973
SEQUENCE DESCRIPTION: SEQ ID NO: 4810:
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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4810, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: CD/ROM ISO9660
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OPERATING SYSTEM: <Unknown>
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TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 973 amino acids TYPE: amino acid
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STATE: Massachusetts
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COMPUTER READABLE FORM:
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TYPE: PRT
ORGANISM: Artificial Sequence
                                            APPLICANT: HASELKORN, ROBERT
                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
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                                                                                                    SMKKVLVANRGEIAVRVFRACTELGIKTVGIYAEKNEYSVHRFKADEAYLVGQGKKPIDA 70
                                                                                 28 AFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKA 87
                                                                                                                                                                                                                                                     207 LATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVV
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                            Length 973;
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                            37.2%; Score 2182; DB 4;
llarity 48.1%; Pred. No. 5.4e-164;
Conservative 143; Mismatches 320;
                                         Similarity
US-09-107-532A-4810
                                                   455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 KILVANRGEIPIRIFRTAHELSMQTVAIYSHEDRLSTHKQKADEAYVIGEVGQYTPVGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 ATEASREABEAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 KILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEG--SPVKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 IOMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDAVLFTNT
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                                                                                                             APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-66-07
PRIOR FILING DATE: 1995-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARR: PATENTIN Ver. 2.1
SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.3%; Score 1192; DB 4; Length 694; Best Local Similarity 27.9%; Pred. No. 8.9e-86; Matches 316; Conservative 102; Mismatches 239; Indels 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description of Artificial Sequence:
Peptide
Sequence 126, Application US/09433043B Patent No. 6399342 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492
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qa	492 491	Db 131 AGADLFADLHLPQQDALRENGAAIQCRITTEDPENNFMPDIGTI
QY	747 ALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSAIVAAFA 806	QY 401 AAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSC
qa	492 491	Db 191 NAYAGAVVSPYFDSILVKASVHAPSFPAAVAKWQRALHBFQIT
QY	807 HTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGFIGRVYRHEIPGGQLSNLRAQATA 866	Qy 461 FISKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKPHC
qa	492 491	: Db 251 FRIGEAETAFIDAHPELLQVQAKPDIASRLLWYISDVTVNGFK
Qy	867 LGLADRFELIEDNYAAVNEMLGRP-TKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYD 925	QY 520 IKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVIDTIFRE
qq	492DNGSSIKGQLGLPRLKSNPSVPHSYN 517	Db 309 TRHFAAAKPQTDLVALLKNEGAQAVIDWVKAHPALLIJDITFRI
, QY	926 IPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADDSKERRN 985	QY 577 PAAEAVAKLIPELLSVEAMGGATYDVAMRILEEDPWDRLDELI
qq	518 517	Db 369 TVAEDMGNGLPNLFSMEVWGGATFDVAXRFLNEDPWVRLKKLRR
- 0γ	986 SLNRLLFPKPTEEFLEHRRREGNTSALDDREFFYGLVEGRETLIRLFDVRTPLLVRLDAI 1045	Qy 637 VGYTPYPDSVCRAFVKEAASSGVDIFRI 664
qq	518MYPRVYEDFQKMRETYGDLSVLPTRSFLSPLETDEEIEVVIEQGKT-LIIKLQAV 571	Db 429 VGYQNYPDNVIKAFINQAANDGVDVFRI 456
- qa	1046 SEPDDK-GMRNVVANVNGQIRPMRVRDRSVESVTATABEKADSSNKGHVAAPFAGV-VTVT 1103 572 GDLXKRTGRREVVFDI.MCRMRKTRVANRSORVFTVTV KARAMENTER VAN SORVETVOR 103	RESULT 8
Qy	VAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVV 1156	Sequence 122 Application US/09433043B ; Patent No. 6399342
qa	632 VHKGSLIKKGOPVAVLSAMKMEMIISSPSDGQVKEVFVSDGENVDSSDLLVLL 684	; GENERAL INFORMATION: ; APPLICANT: HASELKORN, ROBERT ; ADDITORNY: ADDITIONED
RESULT 7 US-09-63	RESULT 7 US-09-634-238-276	; TILL CONTROLLON: CANOBACTERIAL AND PLANT ACETYL-CONTROLS REFERENCE: ARCD:338US ; CURRENT APPLICATION NUMBER: US/09/433.043B
; Sequer ; Patent . GENEED	Sequence 276, Application US/09634238 Patent No. 654472 FOREMAN TOWN	; CURRENT FILING DATE: 1999-10-25; PRIOR APPLICATION NUMBER: 08/475,879
APPLICANT ; APPLICANT	CANT: Glenn, Matthew CANT: Havukkala, Ilkka J.	FRIOR FILING DATE: 1995-06-0/ PRIOR PAPLICATION NUMBER: 07/956,700 PRIOR FILING DAME: 1003-10-03
; APPLICANT ; APPLICANT		; NUMBER DEFENDED STORY STORY STORY SECTION STORY SECTION SECT
; APPLICANT ; APPLICANT	: Dekker, C	; SEQ 1122 ; SEQ 122 ; TENDER : 603
; APPLICANT; APPLICANT	: Holland, Ross : O'Toole, Paul W.	; TYPE: PT: 7: 7: 7: 7: 7: 7: 7: 7: 7: 7: 7: 7: 7:
; APPLICANT	lian R. , Timothy	FEATURE: CHER INFORMATION: Description of Artificial Sequence
; TITLE ; TITLE . FILE	TITLE OF INVENTION: Polynucleotides, materials incorporating TITLE OF INVENTION: them and methods for using them.	
; CURRE	Ξ ?	Query Match 17.7%; Score 1039.5; DB 4; Le Best Local Similarity 44.3%; Pred. No. B.4e-74;
; NUMBI	.R OF SEQ ID NOS: 422 'ARE: FastSEQ for Windows Version 4.0	les 229; Conservative 80
; SEQ ID NO ; LENGTH:	NO 276 TH: 456	Oy 29 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFR
ORG	TIPE: PAT TACTODACILLUS THAMNOSUS	
39-60-SD		Qy 89 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIC
Query Match Best Local	18.5%; Score 1084; DB 4; Length 456; Similarity 51.3%; Pred No. 1.6e-77;	62
Ma LCIDE Ov	230; CODSEEVATIVE bb; Mismatches 142; Indels 10; Gaps	149
7 원	12 MYVEKYIASAKHVEVQVLGDEHGHLHLEFERCSVQRROKVVVETARPALPLALARNIC 71	DD 122 EIMQKAGVFIVFGSEGLVEIEGEGLELAKDIGKFVMIKAT OV 204 IRKIATFASPEARAAFGDGSGVVFRAVINDOHIEVOILGDRTGE
QY	EMNPRIQVEHTVTEEVTEVDLVKAQMRLA	178
qu	72 QSAVDLMASLHYENAGTVEFLVD-GDQYYFIEVNPRVQVEHTITELITGVDIVQSQLRIA 130	QY 264 KVVETAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLYDE
QY	344 AGATL-KELGL-TQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLD-G 400	Db 238 KLLEEAPSPALDSDLREKMGQAAVKAAQFINYAGAGTIEFLLDR

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/SGVATNIGELRALLRED 460
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!TGVKTNVAFLEHLLATQT 250
                                                                 HGV-RPKDVAAPIDKLPN 519
                                                                               LREAMPNVNIQMLLRGRNT 636
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YGPTPEAIRLMGDKSTAK 121
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| |:|| ||||||:||
GNVIHLGERDCSIQRRNQ 237
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|LADEAVCIG-EPASAKSY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  indels 31; Gaps
                                                                                                                                                                                                                                                                                                          COA CARBOXYLASE
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29 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY	OY 204 NVEARAGEMENT CALON RELEASELY MELLONG STATE TEARNET TO THE STATE OF S	RESULT 10 US-08-422-560A-6 SGGUENCE 6, APDICATION US/08422560A SGGUENCE 6, APDICATION: PAPLICANT: Haselkorn, Robert APPLICANT: Haselkorn, Robert APPLICANT: Garnicki, Piotr TITLE OF INVENTION: ACETYL-COA CARBOXYIASE COMPOSITIONS AND TITLE OF INVENTION: MATHODS FOR USE NUMBER OF SEQUENCES: 31 CORRESPONDENCES: 31 CORRESPONDENCES: 31 CORRESPONDENCES: 31 CORRESPONDENCES: 31 CORRESPONDENCES: 31 CORPUTER IN FO. Dox 4433 COMPUTER IN FO. Dox 4433 COMPUTER FIABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE CORPUTER: IAP PC COMPATIBLE COMPUTER: IAP PC COMPATIBLE COMPUTER: IAP PC COMPATIBLE COMPUTER: IAP PC COMPATIBLE COMPUTER: IAP PC TOS/MS 100 SOFTWARE: PATENTION NUMBER: US 007 956,700 FILING DATE: U1-APR-1992 ATTORNEY/AGENT INFORMATION: NAME: Wilson, MATA: RESISTENCE/COKET UNBER: 37,259 RESERRENCE/COKET UNBER: 37,259 RESERRENCE/COKET UNBER: 37,259 RESERRENCE/COKET UNBER: ABCD:152/WIM TELEDRHONE: 512-418-3000	; INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: ; LENGTH: 447 amino acid; TYPE: amino acid
QY 324 HTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCKITTEDPNNGFRPDTG 383	- ZZZZGGGGGGGG	6 Y DA COAR A COAL COAL COAL COAL COAL COAL COAL CO	Query Match 17.6%; Score 1032.5; DB 1; Length 447; Best Local Similarity 48.2%; Pred. No. 1.9e-73; Matches 216; Conservative 71; Mismatches 148; Indels 13; Gaps 4;

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384 IITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVS 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 LRKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQ 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 KVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 HIVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 TAAKKAGLPVLAES-----TPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 RISGYLPPGGPGVRIDSHVYTDYQIPPYYDSLIGKLIVWGPDRATAINRMKRALRECAIT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 FDKILIANRGEIALRILRACEEMGIATIAVHSTVDRNALHVQLADEAVCIG-EPASAKSY
                                                                                                                                                                                                                                                                                                                                                                          Length 447;
                                                                                                                                                                                                                                                                                                                                                                        17.6%; Score 1032.5; DB 3; Length 48.2%; Pred. No. 1.9e-73; Live 71; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING TITLE OF INVENTION: ACETYL-COA CARBOXYLASE AND USES TITLE OF INVENTION: THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 GVATNIGFLRALLREEDFTSKRIATGFI 471
                                                                                                         REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
   JMBER: PCT/US93/09340
30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Arnold, White & Durkee P.O. Box 4433
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Patent No. 5801233
                                                      ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
                                                                                                                                                 TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                        9
                                                                                                                                                                                                                                           LENGTH: 447 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.2%
Matches 216; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                  single
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 APPLICATION NUMBER:
FILING DATE: 30-SEP
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                    89 I.DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 148
                                                                                                                                                                                                                                           264 KUVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVE 323
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                                                                                                                                                                                                                                                                                                                                                                      204 LRKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQ 263
                                                                                                                                              29 FKKILVANRGELAVRAFRAALETGAATVALYPREDRGSFHRSFASEAVRIGTEGSPVKAY 88
                                                                                                                                                                               3 FDKILIANRGEIALRILRACEEMGIATIAVHSTVDRNALHVQLADEAVCIG-EPASSAKSY 61
                                                                                                            13; Gaps
                                                                    17.6%; Score 1032.5; DB 2; Length 447; 48.2%; Pred. No. 1.9e-73; tive 71; Mismatches 148; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Sequence 6, Application US/08468793
/ Patent No. 6177267
/ GENERAL INFORMATION:
    APPLICANT: Haselkorn, Robert
    APPLICANT: Gornick!, Piotr
    TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
    TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS/ASCII
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 GLPITIGEHQRIMENPQFLQGNVSTSFV 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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CLASSIFICATION: 800
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                                                                      Query Match 17.6%
Best Local Similarity 48.2%
Matches 216; Conservative
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CITY: Houston
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
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                                   US-08-422-560A-6
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US-08-422-560A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 453;
                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: CAPPLICATION NUMBER: US/08/611.107 FILING DATE: CONCURRENTLY Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 17.1%; Score 1005.5; DE similarity 47.1%; Pred. No. 2.7e-71209; Conservative 72; Mismatches 15
                                                                                                                                                                                                                                                                                                                   US PCT/US93/09340
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US N 07/956,700
FILING DATE: 02-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/0934(
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US SN 08/422,560 FILING DATE: 14-APR-1995 ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33,928
REFERENCE/DGCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
                    United States of America
                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
                                                                            Floppy disk
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TYPE: amino acid
STRANDEDNESS:
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                                                       COMPUTER READABLE FORM:
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US-08-611-107-8
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COUNTRY: Un. 77210
                                                                              TYPE:
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Best Local
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RESULT 13

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89 IDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 148
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                                                                                                      ACETYL-COA CARBOXYLASE COMPOSITIONS AND METHODS FOR USE
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                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.1%; Score 1005.5; DB 47.1%; Pred. No. 2.7e-71; Live 72; Mismatches 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/422,560A
FILING DATE: 14-APR-1995
                                                                                                                                                                                           E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/956,700 FILING DATE: 02-0CT-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
Sequence 8, Application US/08422560A Patent No. 5910626
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
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TELEPHONE: 512-418-3000
                                                          APPLICANT: Haselkorn, Robert
APPLICANT: GOTAICKI, PIOLT
TITLE OF INVENTION: METHODS I
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                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
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TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                               NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Wi
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US-08-422-560A-8
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                                          GENERAL INFORMATION:
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COUNTRY:
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208 ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVE 267
                                                                                     182 FLAAQGEAEAAFGNPGLYLEKFIDRPRHVEFQILADAYGNVVHLGERDCSIQRRHQKLLE 241
                                                                                                                                                      388 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 447
        122 ETMQRVGVPTIPGSDGLLTDVDSAAKVAAEIGYPVMIKATAGGGGRGMRLVREPADLEKL 181
                                                                                                                              268 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 327
                                                                                                                                                                                                              EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GORNICKI, FIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD: 33805
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR PILING DATE: 1995-06-07
PRIOR PELICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
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ullarity 47.1%; Pred. No. 3.9e-71;
Conservative 72; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                  : | : : | : | | : 419 TLSFHQLMLQMPEFLRGELYTNFV 442
                                                                                                                                                                                                                                                                                                                                                                             448 NIGFLRALLREEDFTSKRIATGFI 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 121, Application US/09433043B
Patent No. 639342
SENERAL INFORMATION:
PAPLICANT: HASELKORN, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.1
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US-09-433-043B-121
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359 YLPPGGPGVRVDSHVYTDYEIPPYYDSLIGKLIVWGATREEAIARMQRALRECAITGLPT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 TAAKKAGLPVLAESTP-SKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
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                                                                                                                                                                                                                                                                                     ACETYL-COA CARBOXYLASE COMPOSITIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.1%; Score 1005.5; DB 47.1%; Pred. No. 2.7e-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US SN 07/956,700 FILING DATE: 02-007-1992
APPLICATION: 800 APPLICATION NUMBER: PCT/US93/09340
                                      448 NIGFLRALLREEDFTSKRIATGFI 471
                                                                19 TLSFHQLMLQMPEFLRGELYTNFV 442
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/422,560 FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JMBER: US/08/468,793
06-JUN-1995
                                                                                                                                                                                Sequence 8, Application US/08468793
Patent No. 6177267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARC
                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1993
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                                                                                                                                                                                                                                                                                                                             53
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                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              800
                                                                                                                                                                                                                                                                                                                           NUMBER OF SECUENCES:
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                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: PatentI
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Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                Texas
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Texa COUNTRY: Un ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-468-793-8
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g δy q ŏ

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        QY
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        DD
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Search completed: September 24, 2003, 15:43:53 Job time: 22.1332 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 24, 2003, 15:41:22; Search time 36.7701 Seconds Run on:

(without alignments)
4760.992 Million cell updates/sec

US-09-974-973A-2 5865 Perfect score: Title:

1 MTAITLGGLLLKGIITLVST.......RVVVPAATKVEGGDLIVVVS 1157 Sedneuce:

Scoring table:

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Total number of hits satisfying chosen parameters:

566894 seqs, 151307093 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

Published_Applications_AA:*

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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:* 110. 111. 111. 111. 112. 113. 114. 118. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

Description	Sequence 2, Appli	Sequence 4, Appli		Sequence 4265, Ap	Sequence 2, Appli	Sequence 5468, Ap	Sequence 10806, A	Sequence 12361, A	Sequence 6, Appli	Sequence 8, Appli	Sequence 5215, Ap	Sequence 13885, A	Sequence 11160, A	Sequence 14226, A	Sequence 10330, A
ΩI	US-09-974-973-2	US-09-974-973-4	US-09-974-973-19	US-09-738-626-4265	US-10-045-072-2	US-09-815-242-5468	US-09-815-242-10806	US-09-815-242-12361	US-09-767-479-6	US-09-767-479-8	US-09-815-242-5215	US-09-815-242-13885	US-09-815-242-11160	US-10-156-761-14226	US-09-815-242-10330
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% Query Match	100.0	100.0	98.2	98.2	98.2	42.4	42.0	39.2	17.6	17.1	16.7	16.3	16.2	16.0	16.0
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Result No.	1	7	m	4	S	9	7	80	o	10	11	12	13	14	15

Sequence 13617, A	Sequence 13364, A	٠.	, ,	Sequence 10874, A	963,	4	Sequence 25, Appl	Sequence 11558, A		Sequence 2, Appli					5418	Sequence 12562, A	5806	1312	114	Sequence 28, Appl	Sequence 12939, A	Sequence 10, Appl	Sequence 8, Appli	Sequence 1328, Ap	Sequence 5, Appli	Seguence 5031, Ap		Sequence 20, Appl	240,
9 US-09-815-242-13617	US-09-815-24	US-09-815-24	US-09-815-24)-156-76				_							_	0S-05	US-09-815	US-09-815-242-131	US-10-15	US-10-169-048-26	US-09-815-24	US-09-767-479	US-09-839-47	15 US-10-083-357-1328	5 US-10-224-539A-	9 US-09-815-242-5031	0 US-09-895-913A-	$6 ext{ } US-10$	9 US-09-205-658-240
455	455	449	458	590	443	456	590	455	725	725	725	290	700	591	446	453	448	451	616	464	358	2257	2257	483	262	. 158	163	1073	124
16.0	16.0	15.7	15.7	15.5	15.5	15.5	15.4	15.4	15.3	15.3	15.3	15.2	15.2	15.0	14.6	14.6	14.3	14.2	14.1	11.1	10.8	6.6	9.1	7.5	7.2	6.4	5.1	4.3	4.3
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16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 2, Application US/09974973

Sequence 2, Application US/09974973

Patent No. US20020177202A1

GENERAL INFORMATION:

TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter

FILE REPRESENCE: 1553.1230001/MAC/RGM

CURRENT APPLICATION NUMBER: US/09/974,973

CURRENT FILING DATE: 2001-10-21

PRIOR APPLICATION NUMBER: US 60/239,913

PRIOR FILING DATE: 2000-10-13

NUMBER OF FILING DATE: 2000-10-13

NUMBER OF SEQ. ID NOS: 19

SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTY 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIFVKAVAGGGGRGMRFVSSPDELRKLATEASREAERAFGDGSVYVERAVINPQHIEVQI 240
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                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 5865; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                              TYPE: PRT Organism glutamicum
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US-09-974-973-2
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qa	181	PIFVKAVAGGGGRGMRFVSSPDELRKLATEASREAEAAFGDGSVYVERAVINPOHIEVOI 240	
δλ	241	301	
qq			
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ΟŊ	361	GAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKWT 420	
qa	361	NGFRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFI	76-60-SU
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QQ	1141	VPAATKVEGGDLIVVVS 1157	qa
E 1110 G C	c		Qy
TG-00-C	2 974-973-		,

Sequence 4, Application US/09974973 Patent No. US20020177202A1

US-09-974-973-4

APPLICANT: Hanke, Paul D. ; Sequence 4, Applicati
; Patent No. US20020177
; GENERAL INFORMATION:
; APPLICANT: Hanke, Pa

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LE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter REPERENCE: 153.1230001/MAC/RGM
RENT APPLICATION NUMBER: US/09/974,973
RENT FILING DATE: 2000-10-21
DR APPLICATION NUMBER: US 60/239,913
DR FILING DATE: 2000-10-13
BER OF SEQ. ID NOS: 19
IWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 HGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMT 420
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                                                                                                                                                                                                                                   ANISM: Corynebacterium glutamicum
                                                                                                                                                                                          GTH: 1157
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QY 378 FRPDTGTITATRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRAL 437 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 558 FRDAHOSLLATRVRSFALKPAABAVAKLTPELLSVEAWGGATYDVAMRFLÆEDPWDRLDE 617 Db 541 FRDAHQSLLATRVRSFALKPAABAVAKLTPELLSVEAWGGATYDVAMRFLÆEDPWDRLDE 600 QY 618 LREAMPRVNIQMLLRGRYTVGYTPYPPSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA 677 Db 601 LREAMPRVNIQMLLRGRYTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA 660	QY 678 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR 737 111111111111111111111111111111111111		QY 918 AADPQXYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEBEQAHLDA 977 DD	QY 1038 LLVRLDAISEPDDKGMRNVVANVNGQIRFMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1097	RESULT 4 US-09-738-626-4265 Sequence 4265, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION: APPLICANT: NAKAGMA, SATOSHI APPLICANT: ANDO, SEIKO APPLICANT: HAYASHI, MIKIRO APPLICANT: HAYASHI, MIKIRO APPLICANT: TATEISHI, MIKIRO APPLICANT: TATEISHI, MIKIRO APPLICANT: TATEISHI, NACOC APPLICANT: SERDA, MASATO APPLICANT: OZAKI, AKIU TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERBNCE: 249-125 CURRENT FILING DATE: 2000-12-18
QY 841 PGPTGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVV 900 DD 841 PGPTGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVV 900 QY 901 GDLALHLVGAGQDPADFAADPQKYDIPDSYIAFLRGEIGNPPGGRPEPLRYRALEGRSEG 960 QY 901 GDLALHLVGAGVDPADFAADPQKYDIPDSYIAFLRGEIGNPPGGWPEPLRYRALEGRSEG 960 QY 961 KAPLTEVPEEEQAHLDADDSKERRNSLLRPRKPGELGHPRGGWPEPLRYRALEGRSEG 960 QY 961 KAPLTEVPEEEQAHLDADDSKERRNSLLRPRKPGPTGSTERRRRGUTSALDDREFYG 1020 Db 961 KAPLTEVPEEEQAHLDADDSKERRNSLNRLLFPRKPTEEFLEHRRRGUTSALDDREFYG 1020 Db 961 KAPLTEVPEEEQAHLDADDSKERRNSLNRLLFPRKPTEEFLEHRRRGUTSALDDREFYG 1020	QY 1021 LVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTAT 1080 DD 111111111111111111111111111111111111	QY 1141 VPAATKVEGGDLIVVVS 1157 Db 1141 VPAATKVEGGDLIVVVS 1157 RESULT 3 US-09-974-973-19	; Sequence 19, Application US/09974973 ; Patent No. US20020177202A1 ; GENERAL INFORMATION: APPLICANT: Hanke, Paul D TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacterium FILE REFERENCE: 1533.1230001/NAC/RGM CURRENT TAPLICATION NUMBER: US/09/974,973 CURRENT TILING DATE: 2001-10-21 PRIOR APPLICATION NUMBER: US 60/239,913	o, o	Query Match Best Local Si Matches 1133; Y 18 V	QY 78 IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV 137 b

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LLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1097
                                                                                                                                                                                                   1021 LLVRLDAISEPDDKGMRNVVANVAGIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1080
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Publication No. US20030027305a1
| GeneRal Information:
| APPLICANT: Sinskey, Anthony J. |
| APPLICANT: Lessard, Philip A. |
| APPLICANT: Mills, Laura B. |
| TITLE OF INVENTION: PYTUVATE Carboxylase from Corynebacterium glutamicum FILE REFERENCE: 1533 0790002
| CURRENT APPLICATION NUMBER: US/10/045,072
| CURRENT FILING DATE: 2002-01-15
| PRIOR APPLICATION NUMBER: US 09/677,575
| PRIOR FILING DATE: 1900-10-03
| PRIOR FILING DATE: 1900-10-03
| PRIOR FILING DATE: 1998,12-23
                                                                                            SNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF
                                         918 AADPOKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDA
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5; Mismatches
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Best Local Similarity 99.4%;
Matches 1133; Conservative
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Pred. No. 0;
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                      Corynebacterium glutamicum
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Best Local Similarity 99.4%;
Matches 1133; Conservative
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                                                                                                         SEQ ID NO 4265
LENGTH: 1140
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-1127
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                ; ORGANISM: Staphylococcus aureus US-09-815-242-5468
                                                                                                                                                                                                                                    SEQ ID NO 5468
                                                                                                                                                                                                                                                        LENGIH: 1147
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                 FRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRAL
                                                                                                                                         TVNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTT
                                                                                                                                                         FRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDE
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APPLICANT: Haselbeck, Robert
APPLICANT: Apsilon, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamancto, Robert T.
APPLICANT: Yamancto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROKARYOTES
FILE REPRESENCE: ELITRA.011A
TITLE REPRESENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078 Sequence 5468, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: -09-815-242-5468

14; 244 APSVGLSPTLRQRICDAAIQLMENIKYVNAGTVEFLVSGDE---FFFIEVNPRVQVEHTI 300 90 DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149 150 AAKKAGLPVL-AESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLA 208 209 TEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI 268 384 TITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV 442 361 TIIAYRSSGGFGVRLDAGDGFQGAEISPYYDSLLVKLSTHAISFKQAEEKMVRSLREMRI 420 -RGSRDRLKQLGPAAFARD 544 545 LREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAM 604 443 SGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKP APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLV--DEKGNHVFIEMNPRIQVEHTV 30 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL TEEVTEVDLVKAQMRLAAGATL - - KELGLTQDK - IKTHGAALQCRITTEDPNNGFRPDTG ------GFPNVEKRPKPDYELASIPTVSSSKIASFSGTKQLLDEVGPKGVAEW RFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRI FDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDP-NEKLYTLDYYLKMAEEIVKSG Gaps 503 HGVRPKDVAAPIDKLPNIKDLPLP 421 479 605 999 엄 QΥ g Qγ g δy qq δŽ

Query Match 42.0%; Score 2460.5; DB 9; Length 1142; Best Local Similarity 45.5%; Pred. No. 5.9e-188; Matches 529; Conservative 187; Mismatches 387; Indels 59; Gaps 17;	QY 30 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASBAVRIGTEGSPVKAYL 89 :	QY 90 DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGFTPEVLDLIGDKSRAVT 149	QY 150 AAKKAGLPVLAEST-PSKNIDDIVKSAEGQIYPIFVKAVAGGGGRGMFVSSPDELRKLA 208 	QY 209 TEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI 268	QY 269 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVGFLVDEKGNHVFIEMNPRIQVEHTVTE 328 :-	QY 329 EVTEVDLVKAQMRLAAGATL-KELGL-TQDKIKTHGAALQCRITTEDPNNGFRPDTGTIT 386 301 MITDIDIVISQLQIAQGLDLHKDMHLPKQNELTLKGAAIQCRITTEDPLNQFMPDTGKID 360	QY 387 AYKSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGV 445	QY 446 ATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKPHGV 505	QY 506 RPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAFARDLREQDALAV 553	QY 554 TDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFE 609	QY 610 DPWDRLDELREAMPHVNIQMLLRGRHTVGYTPYPDSVCRAFVKEAASSGVDIFRIEDALN 669 	QY 670 DVSOMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAI 729 :	OY 730 KDWAGLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPL 789	OY 790 SGITSQPSLSAIVAAFAHTREDIGLISLEAVSDLEPYWEAVRGLYLPFESGIPGPIGRYR 849	QY 850 HEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVG 909	QY 910 AGVDPADFAADPOKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPE 969 1 : : : : :	Qy 970 EEQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRFGNTSALDDR 1015	QY 1016 EFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVE 1075
Qy 724 AHILAIKDMAGLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLAIYFAAAQAGADAVD 783 	QY 784 GASAPLSGTTSQPSLSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGP 843 	Qy 844 TGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDL 903 : : :	QY 904 ALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAP 963	QY 964 LTEVPEERQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRFGNTSAL 1012	QY 1013 DDREFPYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRFMRVRDR 1072	QY 1073 SVESVTATAEKADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITAS 1131	Qy 1132 VDGKIERVVVPAATKVEGGDLIVVV 1156	RESULT 7 US-09-815-242-10806 : Sequence 10806 Application US 700915232	; Patent No. 0520020061569A1 ; GENERAL INFORMATION: ; APPLICANT: Haselbeck, Robert	APPLICANT: CALLELY, NAIL W. APPLICANT: Wall, Daniel APPLICANT: Waxek, John D. APPLICANT: Carr, C	<u>.</u> 2	REFERENCE: ELITH NT APPLICATION N NT FILING DATE: APPLICATION NIM	PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727		FILING DATE: 2000-11-27 APPLICATION NUMBER: 60/257,93 FILING DATE: 2000-12-22 APPLICATION NUMBER: 60/55930			

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11	qa XX	99 LDA 57 REE
TVDHIYVEEGFAISSGDLLLEV 1139 12361	Db Qy Db	359 KNKKFISGDYTTKFIETPELFDIQPSLDRGTKTLEYIGNYIN
Sequence 12361, Application US/09815242 Patent No. US20020061569A1 APPLICAWT: Haselbeck, Robert ADDITCAMM: Chicae R. Robert	o dy	
	QY GD	619 REAMPHVNIQMILKGRHTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAI : :
of Essential Genes in	QY	679 DAVLETNTAVAEVAMAYSGDLSDP-NEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR:
.: US/09/815,242 -: US/09/815,242 -: 03-21	Qy Dp	738 PAAVTKINTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPS
FILING DATE: 2000-03-21 APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23 APPLICATION NUMBER: 60/206,727	QY Db	798 LSAIVAAFAHTREDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL :::
FILING DATE: 2000-05-26 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253 625	oy do	858 SNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVIPSSKVVGDLALHLVGAGVDPADF
FILING DATE: 2000-11-27 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22 APPLICATION NUMBER: 60/269,308	QY Db	918 AADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLIEVPEEQAHILDA
ING DATE: 2001-02-16 SEQ ID NOS: 14110 FastSEQ for Windows Version 4.0	. Qy	978 DDSKERRNSLNRLLFPKPTEEFLEHRRFGNTSALDDREFFYGLVEGRE : :
	Qy	1027 TLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGGIRPMRVRDRSVESVTATAEKADS
Score 2300; DB 9; Length 1073; Pred. No. 4e-175;); Mismatches 360; Indels 62; Caps 14;	QY	1087 SNKCHVAAPFAGVVT-VIVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAAT
104 DAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLIGDKSRAVTAAKKAGLPVL-AES 162 	OY Db	1146 KVEGGDLIVVV 1156 : ::: 1058 TIATGDLLIEI 1068
TPSKNIDDIVKSAEGQTYPIFVKAVAGGGRGMRFVSSPDELRKLATEASREAEAAFGDG 222 :	S-S	T 9 -767-479-6 uence 6, Application US/09767479
SVYVERAVINPQHIEVQILGBRIGEVVHLYERDCSLQRRHOKVVETAPAQHLDPELRDRI 282 : : : :: :	1	SZUULUJ6654Al FORMATION: ZANT: Haselkorn, Robert Gornicki, Piotr
CADAVKFCRSIGYQGAGTVEFLVDEKGNHYFIEMNPRIQVEHTYTEEVTEVDLYKAQM 340 :: :		, i
341 RLAAGATLKELGLTQDK-IKTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVR 397	_	AUDKESSEE: Arnold, White & Durkee STREET: P.O. Box 4433

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89 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLIGDKSRAV 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS/ASCII
OPERATING SYSTEM: Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.6%; Score 1032.5; DB 9;
48.2%; Pred. No. 4.1e-74;
Live 71; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: ARCD:152/KIT
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US SN 07/956,700 FILLING DATE: 02-07-11992 APPLICATION NUMBER: PCT/US93/09340 FILLING DATE: 30-5EP-1993
                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/767,479
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: | ||| :: | :: | CLPTIGEHORIMENPOFLOGNVSTSFV 442
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                                                                                                                                                                 FILING DATE: 22-Jan-2001
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,793
FILING DATE: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
0S-09-767-479-6
                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 447 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6:
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Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ETMQRVGVPTIPGSDGLLTDVDSAAKVAAEIGYPVMIKATAGGGGGRGMRLVREPADLEKL 181
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                                                                                                                           TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/767,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.1%; Score 1005.5; DB 9; 47.1%; Pred. No. 6.1e-72; tive 72; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTOKURIAMEL KITCHELL, BEZDETE S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 38,928
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US SN 07/956,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-0CT-1992
APPLICATION NUMBER: PCT/US93/09340
FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                              STATE: Texas COUNTRY: United States of America
                                                                                                                                                                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-09-767-479-8
                                                                                                                                                  METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 22-Jan-2001
CLASSIFICATION: Unknown
                  Sequence 8, Application US/09767479
Patent No. US20010036654A1
GENERAL INFORMATION:
                                                                                 APPLICANT: Haselkorn, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                         Gornicki, Piotr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                        NUMBER OF SEQUENCES: 29
                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209; Conservative
                                                                                                                                                                                                                                                              CITY: Houston
                                                                                                                                                                                                                                                                                                                        ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
US-09-767-479-8
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OY 205 RKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQK 264	QY 385 ITAXRSPGGAQYRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSG 444	0y 445 VATNIGFTRALLREEDFRENKRALACEIDHHILQ 479 BESULT 12 US-09-815-24-13885 Sequence 13885. Application US/09815242 APPLICANT: OHEROF ALTIL. APPLICANT: OHEROF ALTIL. APPLICANT: Ax manuclo, Nobert T. APPLICANT: Travick, John D. APPLICANT: Travick, John D. APPLICANT: Travick, John D. APPLICANT: Ax manuclo, Nobert T. APPLICANT: Ax manuclo, Nobert T. APPLICANT: Application of Essential Genes in IIILE OF INVERTION: Dentification of Essential Genes in IIILE OF INVERTION: 100-101-201 PRIOR APPLICANTION NUMBER: 06/019, 727 PRIOR APPLICANTION NUMBER: 06/201, 727 PRIOR APPLICANTION NUMBER: 06/201, 727 PRIOR PRILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-02-26 PRIOR FILING DATE: 2000-02-16 PRIOR FILING DATE: 2001-02-16 SED IN 01-1885 LENGHARE: Ad-1:8865	Query Match Best Local Similarity 47.6%; Pred. No. 5.6e-68; Matches 206; Conservative 61; Mismatches 158; Indels 8; Gaps 5;	OY 31 KILVANRGEIAVRAPRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYLD 90
242 SAPARILDPELRDRICADAVKPCRSIGYQGAGTVBFLVDEKGNHVFIEMNPRIQVEHTVT 327 1 1 1 1 1 1 1 1 1	QY 448 NIGFLRALLREDFTSKRIATGFI 471 Db 419 TLSFHQLMLQMPEFLRGELYTNFV 442	RESULT II. SESULT II. SEQUENCE 515, Application US/00815242 Sequence 5215, Application US/00815242 Sequence 5215, Application US/00815242 Sequence 5215, Application US/00815242 Sequence 5215, Application US/00815242 APPLICANT: Tracick, John D. APPLICANT: Tracick, John D. APPLICANT: Carr, Grant J. APPLICANT: Tracick, John D. APPLICANT: Kn. H. Howard ITTLE OF INVENTION: Protatification of Essential Genes in TITLE OF INVENTION: Protation Of Essential Genes in TITLE OF INVENTION: Protation Of Essential CURRENT FILING DATE: 2001-03-219.078 PRIOR FILING DATE: 2000-03-20.191.078 PRIOR FILING DATE: 2000-03-20.191.078 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-10-216 PRIOR PRIOR PRIOR NAMES: 60/269, 308 PRIOR PRIOR PRIOR OF PRIORE: 60/269, 308 PRIOR PRIOR PRIOR DATE: 2000-12-216 PRIOR PRIOR PRIOR DATE: 2000-12-216 SEQUID NO 5215 CORMANISM: Pseudomonas aeruginosa US-09-815-242-5215 GORANISM: Pseudomonas aeruginosa US-09-815-242-5215 Beach Coalservative 14; Mismatches 137; Indels 13; Gaps 6;	QY 30 KKILVANRQEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL 89 	QY 90 DIDELIGAAKKVKADALYDGYGFLSENAQLARECAENGITFIGPTPEVLDLIGDKSRAVT 149 : :: : : :

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DIDELIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149
                                                                                                           150 AAKKAGLPVLAEST-PSKNIDDIVKS---AEGQTYPIFVKAVAGGGGRGMRFVSSPDELR 205
                                                                                                                                                                                                          206 KLATEASREAERAFGDGSVYVERAVINPQHIEVQILGDRIGEVVHLYERDCSLQRRHQKV 265
                                                                                                                                                                                                                                                                                                                                                                                                      EHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                  296 EHPVTEMIIGVDLVKEQLRIAAGL---PISFKQEDIKVKGHAMECRINAEDPKT-FLPSP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV 442
                                                           62 NIPAIIAAAEVTGADAIHPGYGFLSENADFAEQVERSGFTFIGPTADVIRLMGDKVSAIK 121
                                                                                                                                                            122 AMKKAGVPCVPGSDGPVSN--DIAKNKEIAKRIGYPIIIKASGGGGGGRGMRVVRSEDALE 179
                                                                                                                                                                                                                                                                                                         266 VEIAPAQHLDPELRDRI-~-CADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 GKVNHLHSPGGLGVRWDSHVYGGYTVPPHYDSMIAKLITYGDTREVAIRRMONALSETII 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 YLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YLDADLVLKAAKDTGAGAIHPGYGFLSEDAAFARRCEDAGIVFVGFTFEQLELFGAKHTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 VTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RAABEAAGVPLAPGTGLLASLDEALDAASRIGYPVMLKATGGGGGIGMSACRSAAELAES 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRIGEVVHLYERDCSLQRRHQKVVE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVK-A 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.0%; Score 941; DB 15; 28.2%; Pred. No. 4.3e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKRI, YOSHITUKI
APPLICANT: HATTORI NASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERRACE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION UNMER: J002-0-204009
PRIOR APPLICATION NUMBER: J001-204009
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
LD NO 14226
LENNAM: 14226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14226, Application US/10156761
Publication No. US20030119018A1
GENEAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HUSHI
APPLICANT: HORIKAWA, HROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 DGIKTNIPLHELILEDENF 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 SGVATNIGFLRALLREEDF 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-10-156-761-14226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Strep
US-10-156-761-14226
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Best Local 9
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151 AKKAGLPVLAESTPSKNIDDIVKSAEGQT--YPIFVKAVAGGGGRGMRFVSSPDELRKLA 208
                                                123 MKKAGVPTVPGSDGPLGDDMNANRAHAKRIGYPVIIKASGGGGGRGMRVVRSDAELAQSI 182
                                                                                                                                                                                                APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 328
                                                                                                                                                                                                                                                                                             329 EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 388
                                                                                                                                                                                                                                                                                                                                 389 RSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATN 448
                                                                                                                                                                                                                                                                                                                                                                                                                        243 APAPGITPELRRYIGERCAKACVDIGYRGAGTFEFLF-ENGEFYFIEMNTRIQVEHPVTE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EKVVIANRGEIALRILRACKELGIKTVAVHSTADRDLKHVLLADETICIGPAPS-AKSYL 61
                                                                                               209 TEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI
                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.2%; Score 950; DB 9; Length 448; Best Local Similarity 48.3%; Pred. No. 1.7e-67; Matches 212; Conservative 57; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamorto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FITLE OF INVENTION: Proparyotes
FITLE DEPRESSANCE: FITTING OF THE PRESSENTIAL GENES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: U$/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PEPLICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/204,578
PRIOR PELICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11160, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Haemophilus influenzae US-09-815-242-11160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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IDLQTRIMNDEHF 430
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Qy	GYQGAGTVEFLVD-EKGNHVFIEMNPRIQVEHTV	RESULT 15
QO	241 EAPAPGLPSHVRDHLASAARDLCAAVGYRSAGTVEFVYDAAREEAYFLEVNTRLQVEHPV 300	US-09-815-242-10330; Application US/09815242
OY Pr		; Patent NO. USZU02U061589A1 ; GENERAL INFORMATION: ; APPLICANT: Haselbeck.
an a		Ohlsen, Ka
qo Op	357 RVEFPQGVRVDGWVETGTEVTTSYDPMLAKVVANGSDFETAVARAGRALAEFTVSGVA 446 357 RVEFPQGVRVDGWVETGTEVTTSYDPMLAKVVANGSDRAHALARLDEALARTREPVDGIE 414	; APPLICANT: Wall, Daniel ; APPLICANT: Trawick, John D. ; APPLICANT: Grant I
Qy		; APPLICANT: Yamamoto, Robert T.; APPLICANT: Xu, H. Howard
qq	: :	; TITLE OF INVENTION: Identification of Essential Ge; TITLE OF INVENTION: Prokaryotes
Qy Sh	474 HPHILQAPPADDEQGRILDYLADVIVN 500	; FILE REFERENCE: ELITRA.011A ; CURRENT APPLICATION NUMBER: US/09/815,242 ; CURRENT FILING DATE: 2001-03-21
g à	TGAPAPVTVD	; PRIOR APPLICATION NUMBER: 60/191,078 ; PRIOR FILING DATE: 2000-03-21
od da		; PRIOR APPLICATION NUMBER: 60/206,848 ; PRIOR FILLING DATE: 2000-05-23
$Q\bar{Y}$; FALOR AFFILCATION NUBBER: 50/20/,/2/ ; FRIOR FILING DATE: 2000-05-26 ; PRIOR APPLICATION NUMBER: 60/242,578
qa		FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253,
ΟŊ	598 ATYDVPAMRFLFEDP-WDRLDELREAMPNVNIQMLLRGRNTVGYTPYP 643	FILING DATE: 2000-11-27 APPLICATION NUMBER: 60/257,93
qa	649 AGWKVHFNSARIGVRLVGPKPRWARSDGGEAGLHPSNIHDIPYSVGAVDYTGDMPVLLGP 708	; PRIOR FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: 60/269,308
δλ	644 DSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSG 697	LING DATE: 2001-02-16 F SEQ ID NOS: 14110
qa	DGPSLGGFVCPATVATAERWKLG	SOFTWAKE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 10330
δŽ	698 DLSDPNEKLYTLDYYLKMAEBIVKSGAHILAIKDMAGLLRPAAVTKLVTALR 749 : : :	DENGTH: 449 ; TPE: PRT ; ORCANISM: ORCANISM: AND STATEMENT OF STATEMEN
අධ	743PLAEDGSTRPAIVDGGVLARDGDVTYRRSGDDNLLVEFGP 782	10330
Qy Dp	ITSQ	atch 16.0%; Score 940; DB 9; cal Similarity 46.8%; Pred. No. 1.1e-66
}		nes 203; Conservative 66; Mismatc
ස් ස්	/90 PSESAIVAAFAHTRRDTGLSIEAVKSLEPYWEAVRGLYLPFESGTPGPTGRVYRHEI 852 	OY 31 KILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHR
QY	853 PGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVG 901	o
qu	875MAGVRDDAPWCPWNIEFIRRVNGLESVADVYDTVFDAEYLVLGLG 919	63
δδ t	902 DLALHINGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWP 946	QY 151 AKKAGLPVLAESTPSKNIDDIVKSAEGQTYPIFVKA
g a		DD 123 MKKAGVPCVPGSDGPLG-DDMDKNRALAKRIGYPVIIKA
ද්ර අධ	947 EPLRIRALEGRSEGKAPLTEVPEEEQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRFF 1006	QY 208 ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGBRTG
δλ	PDVRTPLLVRLDAISEPDDKGMRNVVANVNGOTR	701
qq		209 LAFAGHLDPELKDRICADANKECKBIGYQGAGTVEFFUDI DD 242 EAPAPGITPELRRYIGERCAKACVDIGYRQAGTFEFFFF-
QY	1066 PMRVRVT 1103	Qy 328 EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQ
qq	1054 AFRARQGAAFAAERDAWEAAGEFARAEAATAPEAPPAEVTVPVGGALVEAEFAASVWQLN 1113	Db 301 EMITGVDLIKEQLRIAAGQPLSIKQEEVHVRGHAVE
ΟŸ	1104 VAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVVS 1157	OY 388 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDF! :

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ITFIGPTPEVLDLTGDKSRAVTA 150
|||| | : | ||| | : |
FIFIGPKAETIRIMGDKVSAIAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDEKGNHVEIEMNPRIQVEHTVT 327
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::||| || || | | | | |
FCRINAEDPNT-FLPSPGKITR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 447 : ::|||: |: | : |: |: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels 10; Gaps
CARPGDQVAAGTALVVLA 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 449;
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357 FHAPGGFGVRWESHIYAGYIVPPYYDSMIGKLICYGENRDVAIARMKNALQELIIDGIKT 416 qq

448 NIGFLRALLREEDF 461 |: ::|:| 417 NVDLQIRIMNDENF 430

δy qq

Search completed: September 24, 2003, 15:53:07 Job time: 44.7701 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 24, 2003, 15:51:53; Search time 35.259 Seconds (without alignments) 3155.707 Million cell updates/sec Run on:

Title: Perfect score:

US-09-974-973A-2 5865 1 MTAITLGGLLLKGIITLVST.....RVVVPAATKVEGGDLIVVVS 1157 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	pornvate carboxvla	Carbowy	Carboxy	carboxy	Carboxy																biotin carboxylase	biotin carboxylase	biotin carboxylase					le biotin c	biotin carboxylase	
SUMMARIES	ID	D70671	A47255	JC4391	A83978	F69685	JC2460	AH1208	AC1565	D97227	G89881	AE2911	C97686	AE3285	T20346	QYBYP	T39734	S46094	T43735	E86708	T44608	D64453	G70427	A70432	A53311	AH1923	D69277	A69123	G82966	874380	
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æ	Query Match	63.3	43.5	43.5	43.2	43.1	3	\sim	$^{\circ}$	$^{\circ}$	$^{\circ}$	$^{\prime}$	42.2	$^{\prime\prime}$	$^{\circ}$	1	1	~~	\leftarrow	41.1	ω ,	8	18.3	~	~	7	17.4	7	16.7	9	
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probable pyruvate	hypothetical prote	biotin carboxylase	biotin carboxylase	hypothetical prote	hypothetical prote	biotin carboxylase	biotin carboxylase	biotin carboxylase	biotin carboxylase	acetyl-CoA carboxy	probable biotin ca	acetyl-CoA carboxy	hypothetical profe	biotin carboxylase	hypothetical prote
7.1	1			vo											
B8347	D87647	B97338	AI0912	F98286	AC2997	C70444	B86722	AD0445	F64105	T07093	H71553	JS0632	D85990	T44813	H91144
2 B8347	2 D8764	2 B97338	2 AI091	2 F9828	2 AC2997	2 C70444	2 B86722	2 AD0445	1 F64105	2 T07093	2 H71553	1 JS0632	2 D85990	2 T44813	2 н91144
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ALIGNMENTS

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1074
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             APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE
                                                     EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY
                                                                                                     RSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATN
                                                                                                                                                                               IGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILLDYLADVTVNKPHGVRPK
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pyruvate carboxylase (EC 6.4.1.1) precursor [similarity] - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Feb-2002
C;Accession: A47255
R;Zhang, J.; Xia, W.L.; Brew, K.; Ahmad, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 1766-1770, 1993

A; Residues: 1-1178 < CERA.
A; Residues: 1-1178 < CERA.
A; Cross-references: GB:L09192; NID:g293743; PIDN:AAA39737.1; PID:g293744
A; Cross-references: GB:L09192; NID:g293743; PIDN:AAA39737.1; PID:g293744
A; Experimental source: 3T3-L1 adipocytes
A; Note: sequence extracted from NCBI backbone (NCBIN:126874, NCBIP:126875)
C; Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi
C; Reywords: biotin binding; ligase; mitochondrion
F;1-20/Domain: transit peptide (mitochondrion) *status predicted <TRP>
F;21-1178/Product: pyruvate carboxylase *status predicted <MAT>
F;39-444/Domain: biotin carboxylase homology <BGH>
F;1105-1178/Domain: lipoyl/biotin-binding homology <LPB>
F;1144/Binding site: biotin (Lys) (covalent) *status predicted domain structure deduc 13; ENAQLARECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVL-AESTPSKNIDDIVK 173 DSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIG 472 GYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGL 353 : | :|:||:||: | :|:|:||: | ::|
663 CEVAKENGMDVFRVFDSLNYLPNMLLGMEAAGSAG-GVVEAAISYTGDVADPSRTKYSLE 721 722 YYMGLAEELVRAGTHILCIKDMAGLLKPAACTMLVSSLRDRFPDLPLHIHTHDTSGAGVA 781 ---FKKILVANRGEIAVRAFRAALETGAA 54 ERADFAQACQDAGVRFIGPSPEVVRKMGDKVEARAIAIAAGVPVVPGTDSPISSLHEAHE TVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLS ||||:| :| | || || || || :||:||||||| || TVAVYSEQDIGQMHRQKADEAYLIGRGLAPVQAYLHIPDIIKVAKENGVDAVHPGYGFLS SAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLATEASREAEAAFGDGSVYVERAVINP 183 FSNTFGFPIIFKAAYGGGGRGMRVVHSYEELEENYTRAYSEALAAFGNGALFVEKFIEKP QHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSI TQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQL-GGEITAHF ENPELFOLRPAQNRAQKLLHYLGHVMVNGPTTPIPVNVSPSPVDPAVPVVPIGPPPAGFR DRLKQLGPAAFARDLREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELL SVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAF 651 VKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLD YYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGOLA DHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRPKDVA-APID-KLPNIKDLPLPRGSR DILLREGPEGFARAVRNHQGLLLMDTTFRDAHQSLLATRVRTHDLKKIAPXVAHNFNKLF Gaps 35; and Best Local Similarity 46.1%; Pred. No. 2.6e-132; Matches 543; Conservative 192; Mismatches 407; Indels A, Title: Adipose pyruvate carboxylase: amino acid sequence A, Reference number: A47255, MUID:93189578; PMID:8446588 A; Accession: A47255
A; Status: preliminary Score 2550.5; DB 1; Pred. No. 2.6e-132; 7 GGLLLKGIITLVSTHTSSTLPA--43.5%; A; Molecule type: mRNA 123 234 22 63 115 174 294 303 354 423 473 483 531 543 Query Match 413 591 603 711 qq ΩD g δ ŏ Qγ g δ δ g ΩŽ qq $\vec{\nabla} \vec{A}$ g δ qq qq ď Q δŽ g δy g QQγ

1105-1178/Domain: lipoyl/blotin-binding homology <lpb> 1144/Binding site: biotin (Lys) (covalent) #status experimental Query Match 43.5%; Score 2548.5; DB 2; Length 1178; Best Local Similarity 46.3%; Pred. No. 3.3e-132; Matches 545; Conservative 188; Mismatches 409; Indels 35; Gaps 1 7 GGLLKGIITLVSTHTSSTLPAFKKILVANRGBIAVRARRALETGAA 54 </lpb>	OY 55 TVAITPREDRGSFHRSFASEAVRIGTEGSPVKAYLDIDBIIGAAKKVKADAIYPGYGFLS 114	OY 174 SAEGGTYPIEVKAVAGGGGRGMRFVSSPDELKKLATEASREAEFAFGDGSVYVERAVINP 233 183 :	QY 294 GYGGGCTVEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGL 353	Db 363 RQENIRINGCAIQCRVTTEDPARSFQPDTGRIEVFRSGEGGGIRLDNASAFQGAVISPHY 422 QY 413 DSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIG 472	QY 473 DHPHILQAPPADDEGGRILDYLABOYTVNKPHGVRPKDVA-APIDKL-PNIKDLPLPRGSR 530 :: : :	QY 591 SVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAF 650 1	QY 651 VKBAASSGYDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAXSGDLSDPNEKLYTLD 710 : : : : : : : : :	1	830 RGLYLPFESGTPGPTGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEML	QY 888 GEFTAVITESSKVGDLALHLYGAGVDPADFAALPQKEDIPUSYLAFLKGELGNPFGGMPE 947 Db 902 GDLIKUTPSSKIVGDLAQFRVQNGLSRAEAEAQAEELSFPRSVVEFLQGXIGIFHGGFPF 961 QY 948 PLRTRALEGRSEGRAPLTEVPEEEQAHLDA-DDSKERRNSLNRLLFFRPTEEFL 1000
QY 770 TYFAAAQAGADAYDGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAV 829 Db 782 AMLACAGGADVVDVAVDSMSGTTSQPSGGALVACTKGTPLDTEVPLERVEDLEFYFINE QY 830 RGLYLPFESGTPGPTGSTSQPSGGALVACTKGTPLDTEVPLERVEDSKYEYEGA 841 QY 842 RGLYLPFESGTPGPTGSTRVYRHETPGGQLSKRAALGLADAFELIEDNYAAVNEML 887	QY 948 PIRTRALEGRSEGRAPLTEVPEEDAHLDA-DDSKERRNSLNRLLFPKPTEEFL 1000 11::	1119		revision 25-Apr-1997 #text_change 11-Jan-2002 JC4391; S06440 W.; Cassady, A.I.; Wallace, J.C. 96 and expression of rat liver pyruvate carboxylase.	NA AJIII> EMBL:U36585; NID:g1040973; PIDN:AAC52668.1; PID:g1040974 AJIII>	acDonald, M.J. rat pyruvate carboxylase-encoding cDNA. MUID:96096548; PMID:8522203	ID:9929988	e and amino acid s	conversi	amily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding ds: biotin binding; gluconeogenesis; homotetramer; ligase; mitochondrion omain: transit peptide (mitochondrion) *status predicted <inp> 8/Product: pyruvate carboxylase *status predicted <mat> //Domain: biotin carboxylase homology <bch></bch></mat></inp>

ପ୍ର	962 PFRSKVLKDLPRIEGRPGASLPPLNLKELEKDLIDRHGEEVTPEDVLSAAMYPDVFAQFK 1021	Db 484 GYPGLE	GYPGLE-KTKKPVFDKPPVPKLKLSEPIPDGTKQILDQHGPEGLAKWVKEQKHVLLTDTT 542
Qy	1001 EHRRREGNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANV 1060 :	Qy 558 FRDAHG Db 543 FRDAHG	FRDAHQSILATRVRSFALKPAAEAVAKLTPELLSVEAMGGATYDVAMRFLFEDPWDRLDE 617
oy Od	1061 NGQIRPMRVRDRSVESYTATAEKADSSNKGHVAAPFAG-VVTVTVAAEGDEVKAGDAVAII 1119 	Qy 618 LREAMP : Db 603 LRKKAP	LREAMPNVNIQMLLRGRNTVGYTFYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA 677 :
QY	1120 BAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVV 1156 :	Qy 678 IDAVLE : bb 663 IEAVGE	IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYXLKMAEEIVKSGAHILAIKDMAGLLR 737 : -
RESULT A83978 pyruvate	RESULT 4 A83978 Pyruvate carboxylase pycA [imported] - Bacillus halodurans (strain C-125)	Qy 738 PAAVTK 1 : Db 722 PEAAYQ	PAAVTKLYTALRREFDLPVHYHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPS 797
C;Specio C;Date: C;Accest R:Takam	1-2001	Qy 798 LSAIVA ::: Db 782 ANSLYY	LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 857 :::
Nucleic A; Title A; Refere	Acids Res. 28, 4317-4331, 2000 Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ence number: A83650; MUID:20512582; PMID:11058132	Oy 858 SNLRAQ Db 842 SNLQQQ	SNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF 917 : : : :
A; Statu: A; Molecu A; Residu A; Cross-		Qy 918 AADPQK : 1 Db 902 YENGHK	AADPQKXDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDA 977 :
A; Exper: C; Geneti A; Gene:	imental source: strain C-125 los: Pyco: Py	QY 978 DDSKER : Db 958 EAIKEE	DDSKER-RNSLNRLLEPKPTEEFLEHRRREGNTSALDDREFFYGLVEGRE 1026
Query Match Best Local Matches 54	Ouery Match 43.2%; Score 2535.5; DB 2; Length 1150; Best Local Similarity 46.9%; Pred. No. 1.7e-131; Matches 540; Conservative 185; Mismatches 399; Indels 77; Gaos 13.	Qy 1027 TLIRLP : : Db 1018 IEVEIE	TLIRLPDVRTPLLVRLDAISBPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADS 1086 ::: :::
Qy Dp	AFKKILVANRGEIAVRAFRAALBTGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPV 85	Qy 1087 SNKGHV 1 Db 1077 SNPNHI	SNKGHVAAPFAG-VVTVIVAEGDEVKAGDAVALIEAMKMEATITASVDGKIERVVVPAAT 1145
QY	86 KAYLDIDEIIGAAKKVRADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKS 145 	Qy 1146 KVEGGLIVVV :: :: Db 1137 AIQTGDLLIEV	LIVVV 1156 :: LIEV 1147
Oy Db	146 RAVTAAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDEL 204 	RESULT 5 F69685 pyruvate carboxylase	(EC 6.4.1.1) pyca [similarity] - Bacillus subtilis
QY	205 RKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLORRHQK 264 :	C;Species: Bacillus C;Date: 05-Dec-1997 C;Accession: F69685 R;Kunst, F.; Ogasawa	~ ~
Qy	265 VVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEH 324	C.; Bron, S.; Brouil A.; Ehrlich, S.D.; E. Nature 390, 249-256, A; Authors: Foulger,	<pre>D, V.; Carter, N.M. Fabret, C.; Ferrari S.; Galizzi, A.; G</pre>
Qy Db	325 TVTEEVTEVDLVKAQMRLAAGATLKELGL-TQDKIKTHGAALQCRITTEDPNNGFRPD 381	<pre>iech, J.; Harwood, C Koetter, P.; Konings A;Authors: Lauber, J Y, M.; Ogawa, K.; Og</pre>	A.; Hullc A.; Lard da, S.; M.; Port
oy Db	382 TGTITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEF 440 	Rieger, M.; Rivolta A;Authors: Schleich, akeuchi, M.; Tamakos T.; Winters, P.; Wipa	Y.; Sato, T. J.; Sekowska, ; Tosato, V.; (; Yata, K.;
yy dd	441 TVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVN 500 1	A; Authors: Yoshikawa A; Title: The complete A; Reference number: A; Accession: F69685	H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. genome sequence of the Gram-Positive bacterium Bacillus subtili 69580; MUID:98044033; PMID:9384377
QY	501 KPHGVRPKDVAAPIDKLPNIK-DLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTT 557 :	A;Status: preliminary; nucleic A;Molecule type: DNA A;Residues: 1-1148 <kun></kun>	.ry; nucleic acid sequence not shown; translation not shown A <kun></kun>

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A. Molecule type: mRNA
A. Residues: 1-1178 < WAL>
A. Molecule type: mRNA
A. Residues: 1-1178 < WAL>
A. Cross-references: BMB: Jouglas, C.; Chen, H.S.; Robinson, B.H.
Biochem. Biophys. Res. Commun. 202, 1009-1014, 1994
A.Title: CDNA cloning of human kidney pyruvate carboxylase.
A. Reference number: JC2460; MUD:94324922; PMID:8048912
A. Reference number: JC2460; MUD:94324922; PMID:8048912
A. Reference number: JC2460; MUD:94324927; PMID:8048912
A. Reference number: JC24, WPP, 227-351, A', 387-485, DV', 488-637, 'R', 639-728, 'A', A', Cross-references: GB:S72370; NID:9632807; PIDN:AAB31500.1; PID:9632808
B. Lamhonwah, A.M.; Quan, F.; Gravel, R.A.
Arch. Biochem. Biophys. 254, 631-636, 1987
A. Reference number: A27883; MUD:97212051; PMID:355348
A. Reference number: A27883; MUD:97212051; PMID:355348
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A; Residues: 1063-1178 <LAM>
A; Biol. Chem. 259, 12831-12837, 1984
A; Title: Molecular cloning of a cDNA for human pyruvate carboxylase. Structural relat A; Reference number: S01469; MUID:85030380; PMID:6548474
A; Accession: S01469
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C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi
                                                                                                                                                                                                                                                                                                                                                                  1079 ATAEKADSSNKGHVAAPFAGVVTVTVAE-GDEVKAGDAVAIIEAMKMEATITASVDGKIE 1137
                                                                                                                                                                                                                                                                                                                                                                                                  1019 YGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVT 1078
                                                               896 EKDVYEKGESLDFPDSVVELFKGNIGQPHGGFPEKLQKLILKGQE----PITVRPGELLE 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pyruvate carboxylase (EC 6.4.1.1) precursor - human
N;Alternate names: pyruvate:carbon dioxide ligase (ADP-forming)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 18-Aug-2000 #text_change 01-Feb-2002
C;Accession: G01933; JC2460; B27883; S01469
R;Walker, M.E.; Jitrapakdee, S.; Val, D.L.; Wallace, J.C.
A;Reference number: H00708
                                  914 PADFAADPOKYDIPDSVIAFLRGELGNPPGGWPEPLRIRALEGRSEGKAPLTEVPEE---
                                                                                                                                                                                                 952 PVSFEAIKQEFKEQHNLEISD----QDAVAYALYPKVFTDYVKTTESYGDISVLDTPFF
                                                                                                                                                                                                                                                                                                         1008 YGMTLGEEIEVEIERGKT-LIVKLISIGEPQPDATRVVYFELNGQPREVVIKDESIKSSV
                                                                                                                                                EQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: biotin binding; gluconeogenesis; ligase; mitochondrion F;1-20/Domain: transit peptide (mitochondrion) #status predicted <TNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;21-1178/Product: pyruvate carboxylase #status predicted <MAT>F;39-494/Domain: biotin carboxylase homology <BCH>F;1105-1178/Domain: lipoyl/biotin-binding homology <LPB>F;1144/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:PC
A;Cross-references: GDB:119472; OMIM:266150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1138 RVVVPAATKVEGGDLIVVV 1156
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A: Residues: 1135-1178 <FRE>
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A;Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13359.1; PID:g2633857 A;Experimental source: strain 168
                                                                                A;Gene: pyca
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 YLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 LATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYERAKSEAKAAFGNDEVYVEKLIENPKHIEVQVIGDKQGNVVHLFERDCSVQRRHQKVI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVN-- 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEEVTEVDLVKAQMRLAAGATL - - KELGLTQDK - IKTHGAALQCRITTEDPNNGFRPDTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 RGIKTNIPFLENVAKHEKFLTGQYDTSFIDTTPELFNFPKQKDRGTKMLTYIGNVTVNGF 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQ 673
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                                                                                                                                                                                                                                                                               Length 1148;
                                                                                                                                 C;Keywords: ligase
F:8-465/Domain: biotin carboxylase homology <BCH>
F:1073-1146/Domain: lipoyl/biotin-binding homology <LPB>
F:1112/Binding site: biotin (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                         43.1%; Score 2530; DB 2;
ilarity 46.0%; Pred. No. 3.3e-131;
Conservative 188; Mismatches 390;
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43.1%; Score 2528.5; DB 1; Length 1178; ilarity 45.9%; Pred. No. 4.2e-131; Conservative 187; Mismatches 415; Indels 35; Gaps 13;	GGLLLKGIITLVSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAA 54 6 	S — S	X 17	INP 23 EKP 24	FCRSI 29 : : LAKQV 30	GYQGAGTVEFLVDEKGNHVF1EMNPRIQVEHTVTEEVTEVDLVKAQMKLAAGATLKELGL 353 	TQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQL-GGEITAHF 412 : : : :	DSMLVKMTCRGSDFETAVARAQRALABETVSGVATNIGFLRALLREEDFTSKRIATGFIG 472 	DHPHLLQAPPADDEQGRILDYLADYTVNKPHGVRP-KDVAAPIDK-LPNIKDLPLPRGSR 530 ::	DRLKQLGFAAFARDLREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPEIJ. 590 	SVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAF 650 	VKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLD 710 	YYLKMABEIVKSGAHILAIKDMAGLLRPAAVTKLYTALRREF-DLPVHVHTHDTAGGQLA 769 : : :	TYFAAAQAGADAVDGASAPLSGTTSQPSLSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAV 829 	RGLYLPFESGTPGPTGRVYRHEIPGGQLSNLRAQATALGLADRFELLEDNYAAVNEML 887 -	GRPTKVTPSSKVVGDLALHLVGAGVDPADFAADFQKYDIPDSVIAFLRGELGNPPGGWPE 947 	RT :
imil '; C	GGLLLK(GGLRLL(TVAIYP] TVAIYS]	ENAQLA] ERADEA(SAEGQT: : FSNTYGI	QHIEVQ:	GYQGAG : GYENAG	TODKIK : : RQENIK	DSMLVKI : DSLLVKI	DHPHLL(::	DRLKQLA 	SVEAWG(: SMENWG(VKEAAS: : CEVAKE	YYLKMA) :: YYMGLA)	TYFAAA(AMLACA(RGLYLP: RGLYAA	GRPTKV: GDLIKV:	PLRTRAI :: PFRSKVI
r Match Local S les 540	7	55 63	115	174	234	303	354 363	413	473	531 543	591 603	651 663	711	770	830	888 902	948
Query M Best Lo Matches	QY Db	QY Db	Qy	Q.Y D.b	, qq	Qy Dp	Qy Db	QY	QY	Qy	Qy Db	Qy Db	Qy Db	Qy Db	oy Db	QY Dp	QY

Pyruvate carboxylase homolog pycA [imported] - Listeria monocytogenes (strain EGD-e) C; Species: Listeria monocytogenes C; Date: 27-Nov-2001 #text_change 14-Dec-2001 C; Accession: AH1208 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Domainguez Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlan, K.D.; Fshhi, D.; Jones, L.M.; Karst, U. Buchrieser, C.; Amend, L.; Dussurget, O.; Entlan, K.D.; Fshhi, D.; Jones, L.M.; Karst, U. Buchrieser, T.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A; Reference number: AB1077; MUID:21537279; PMID:11679669 A; Accession: AH1208 A; Molecule type: DNA A; Residues: 1-1146 cGLA> A; Cross-references: GB:NC_003210; PIDN:CAC99150.1; PID:g16410474; GSPDB:GN00177 C; Genetics: A; Gene 1001 EHRRREGNISALDDREFFYGLVEGRETLIRLPDVRIPLLVRLDAISEPDDKGMRNVVANV 1060 1022 DFTATEGPLDSLNTRLFLOGPKIAEEFEVELERGKT-LHIKALAVSDLNRAGOROVFFEL 1080 1061 NGQIRPMRVRDRSVESYTATAEKADSSNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAII 1119 90 DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149 150 AAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLA 208 125 QALLADIPVIPGSNGPVAGIKEVEEFGEKNGYPLMIKASLGGGGRGMRVVESKEHVKESF 184 209 TEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI 268 269 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 328 304 MITGIDIVQSQLFIADGYALHDQLVAIPKQEDIHIHGSAIQSRITTEDPLNNFMPDTGRV 363 329 EVTEVDLVKAQMRLAAGATLKELGLT---QDKIKTHGAALQCRITTEDPNNGFRPDTGTI 385 386 TAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSG 444 445 VATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKPHG 504 30 KKILVANRGEIAVRAFRAALEIGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAXL 89 5 KKVLVANRGEIAIRVAKRACTELKIKTVAIYSQEDTGSFHRYKSDEAYLVGAGKKPIDAYL 64 Gaps 30; Length 1146; tch 42.5%; Score 2494; DB 2; Length 11 al Similarity 45.7%; Pred. No. 3.2e-129; 525; Conservative 186; Mismatches 408; Indels 1120 EAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVV 1156 Query Match Best Local Matches g g δ δŽ q ă a δŏ 셤 δ g δ d Qy qq δ qq δ g δ

Query Match 42.5%; Score 2491; DB 2; Length 1146; Best Local Similarity 45.9%; Pred. No. 4.7e-129; Matches 527; Conservative 183; Mismatches 409; Indels 30; Gaps 12; Qy 30 KKILVANRGELAVRAFRAALETGAATVATPREDRGSFHRSFASEAVRIGTEGSPVKAYL 89	Db 5 KKVLVANRGEIAIRVMRACTELKIKTVAIYSQEDTGSFHRYKSDEAYLVGACKKFIDAYL 64 QY 90 DIDELIGAAKKVKADAIYPGYGELSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149			QY 269 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVDEFLVDEKGNHVFIEMNPRIQVEHTVIE 328	QY 329 EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTI 385	QY 386 TAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSG 444	QY 445 VATNIGELRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEGGRILDYLADVTVNKPHG 504	QY 505 VRPKDVAAPIDKLENIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVIDTIFRD 560 :::	QY 561 AHQSLLATRVRSFALKPAABAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELRE 620	OY 621 AMPNVNIQMILRGRNIVGYIPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDA 680 1	681 VLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAA	DD 00.2 VREAG-KVVEATICTIGDIDDDTRTRYTIDYXKDMAKELVAQGTHILGIKDMAGLLKPQA 7.20 QY 74.1 VTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSA 800 Db 72.1 stplicerrytvatstrytografians	801 IVAAFAHTREDIGESLEAVSDLEPVWEAVRGLYLPFESGTPGPTGRVYRHEIPGGGLSNL: :		OQQAIAVGLGDRWDEVKEMYTVVNOMFGDIVKVTPSSKVVGDLALFMYQNELTEEDVYEK PQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEE	901	: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
505 VRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTIFRD 560 :::	54.2 AHQSLLATRVRSKDIFQVADAMAHLLPNMFSFEMWGGAIFDVAYRFLNEDEWVRLETLRK 601 621 AMPNVNIQMILRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDA 680 111	681 VLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAA 740 	741 VTKLVTALRREFDLEVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSA 800 	801 IVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLSNL 860 : :	861 RAQATALGLADRFELIEDNYAAVNEMLGRPTKVTESSKVVGDLALHLVGAGVDPADFAAD 920 : : :::	921 PQKYDIPDSVIAFLRGELGNPPGGWPEPLTRALEGRSEGRAPLTEVPEEEQAHLDADDS 980 	981 KBERNSLNRLLFPKPTEEFLEHRRFGNTSALDDREFFYGLVEGRETLI 1029 	1030 RLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNK 1089 	1090 GHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAATKVE 1148 	1149 GGDLIVVVS 1157 :: : 136 SGDLLIEVN 1144		<pre>sarboxylase homolog pycA (imported) - Listeria innocua (strain Clip11262) Listeria innocua n.nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001</pre>	P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker lez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. L.M.; Karst, U.	44, 843-852, 2001 Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mainuerer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Comparative genomics of Listeria species.	A; Accession: Action ACLS55 A; Status: preliminary A; Mesidues: 1-1146 < GTA>	ferences: GB:AL592022, PIDN:CAC96291.1; PID:g16413519; GSPDB:GN00178 ntal source: strain Clip11262	C;Generics: A;Gene: pycA C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Db Db Oy Oy Oy Oy Db Db Db D7227 D97227 D97227 D7227	ELEKGKI-LLIKLNSIGEPIADGTRVIFELNGQPREINIQDMNVQSTY GHVAAPFAG-VYTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKII	ALKPAAEAVAKIJ ALKPAAEAVLA INTUGYTPYPDSV INAVGYTPYPDSV INAVGYTPYPDSV INAVGYRNYPDNN AX SGDLSDPNEKI I I
Query M Best Loo Matches Oy Db Oy Db	atch cal S 519 29 5 5 65	1015 IABGRT-LUVOLLHIGKLDKOGRRN VANVOLRENKUSSYKASSYKATARA TASS 1015 IABGRT-LUVOLLHIGKLDKOGNRTLVFEVNGNRREIKKUKVSSTKSEIVEBIVIADSS 1088 NKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAATK 11 1 1 1 1 1 1 1 1 1
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	149 TAAKKAGLPVL-AESTPSKNIDDIVKSAEGGTYPIEVKAVAGGGGRGREVSSPDELRKL 207	RESULT 10 69981 Dyvavate carboxylase [imported] - Staphylococcus aureus (strain N315) C; Species: Staphylococcus aureus C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C; C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C; Accession: G89881 C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146 A; Reference number: A89758; MUID:21311952; PMID:11418146 A; Residues: Dreliminary A; References: GB:BA000018; PID:q13700915; PIDN:BAB42211.1; GSPDB:GN00149 A; Residues: 1-1150 <

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Q Q

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Pyruvate carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Daces: Marobacterium tumefaciens
C;Dacession: AE2911
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wooderage, G.; Gillet, W.; Grath, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC1; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: circular chromosome
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi
                                                                                                                                                                                                                                                                                                                                                                             Attitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference number: AB2577; MUID:21608550; PMID:11743193
A.Accession: AE2911
A.Status: preliminary
A.Molecule Type: DNA
A.Resiques: 1-1174 <NUR>
A.Cross-references: GB:AE008688; PIDN:AAL43707.1; PID:g17741236; GSPDB:GN00186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 RQLGNKVAARNLAISVDVPVVPATNPLPDDIAEVERMAEEIGYPVMLKASWGGGGRGMRA 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 TVLKISKILVANRSEIAIRVFRAANELGIKTVAIWAEEDKLSLHRFKADESYQVGRGPHL 79
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                                1132 VDGKIERVVVPAATKVEGGDLIVVV 1156
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Best Local Simi
Matches 540;
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61 66 67 72 73 78	PLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRY AFSGNTSQPCLGSIVEALSGSREDTGLDTENIRLSFYWEAVRGLYLPFESGTPGPTGRY I	916 968 972 1016	N-QASSGIDDKGMVTVFFE VT-VTVAEGDEVKAGDAVA :: ISRVFINQGQEVKAGDVLL. 4	RESULT 12 C97686 Pyruvate carboxylase (U51439) [imported] - Agrobacterium tumefaciens (strain C58, Cereon C; Species: Agrobacterium tumefaciens C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Accession: C97686 R; Goodher, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1174 <kur> A;Cross-references: GB:AE007869; PIDN:AAK88444.1; PID:g15157941; GSPDB:GN00169 C;Genetics: A;Gene: AGR.C_4940 A;Map position: circular chromosome C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding</kur>	Query Match Query Match 40.2%; Score 2474.5; DB 2; Length 1174; Best Local Similarity 46.5%; Pred. No. 3.9e-128; Matches 540; Conservative 174; Mismatches 406; Indels 41; Gaps 19; QY 25 TLPAFKKILVANRGEIAVAR-RAALETGAATVAIYPREDRGSFHRSFASEAVRIG 79 DD 20 TULKISKILVANRSEIAIRVFRAANEGIKTVAIWAEEDKLSLHRFKADESYQVGRGPHL 79 QY 80 -TEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVL 138

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A.Map position: 5
A:Introns: 34/3; 103/3; 246/1; 451/3; 567/2; 821/1; 1045/3; 1126/3
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi
C;Reywords: ligase
F;1140/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAHLDA----DDSKERRNS----LNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLV 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     963 AADLDAERKSFEDSVGRKLSDQEFASALMYPKVFTDYATAHETYGPTSVLPTPVYFYGLK 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1023 EGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAE 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1023 PEEEVFVDLERGKTLVIVN-QAMSETDEKGMYTVFFELNGQPRRIKVPNRAKGASGGVRR 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pyruvate carboxylase (EC 6.4.1.1) D2023.2 [similarity] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1083 KADSSNKGHVAAPFAGVV-IVTVAEGDEVKAGDAVAIIEAMKMEAIIIASVDGKIERVVV 1141
                                                                                                                                                                 914 PADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEE--E 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:281052; PIDN:CAB02872.1; GSPDB:GN00023; CESP:D2023.2 A;Experimental source: clone D2023 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 LTIDQIIETALKHNIDAIHPGYGFLSERSDFAAACQNAGIVFIGPSPDVMARMGDKVAAR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 18-Aug-2000
Cispecies: 07346
Fixershaw, J.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219260
A;Reference number: 219260
A;Recession: T20346
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                              MRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMA
                                                                                                                                     GLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTT
                                                                                                                                                                                                                                        SQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIP
                                                                                                                                                                                                                                                                                    SQPCLGSIVEALHGSERDSGLDPDLIRRISFYWEAVRHQYAAFESDLKGPASEVYLHEMP
                                                                                                                                                                                                                                                                                                                                      GGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 FNKVMVANRGEIAIRVFRALTELNKTSVAIYAEQDKNSMHRLKADEAYLVGKGLPPVAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1142 PAATKVEGGDLIVV 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-1175 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: D2023.2
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                                                                                                                                                                                           C;Accession: AE3285
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazor, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: I
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C;Keywords: liqase
                                                                                                                  pyruvate carboxylase (EC 6.4.1.1) [imported] - Brucella melitensis (strain 16M)
C; Species: Brucella melitensis
C; Date: 01-Feb_2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                    A/Residues: Î-1158 <KUR>
A/Cross-references: GB:AE008917; PIDN:AAL51448.1; PID:g17982157; GSPDB:GN00190
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BMEI0266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDK 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EHTVTEEVTEVDLVKAQMRLAAGATL -- KELGL-TQDKIKTHGAALQCRITTEDPNNGFR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BHIVTEEVIGIDIVKAQIHILEGFAIGTPESGVPRQEDIRLNGHALQCRITTEDPEQNFI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDTGTITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALA 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VN-----KPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAV 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQ 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 KILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIG-------TEGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRAVTAAKKAGLPVLAESTP-SKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRKLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.0%; Score 2465.5; DB 2; Length 1158; Best Local Similarity 46.5%; Pred. No. 1.2e-127; Matches 537; Conservative 172; Mismatches 408; Indels 37;
  GKIAEVLVKPGDQIDAKDLLI 1170
                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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1150
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971 EQAHLDADDSK------ERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFY 1019 977 NAKPVDLDAVKVELEEKHGRTLSEEDVMSYSMFPTVFDEFETFRQQYGPVDKLPTRLFLT 1036 1080 TAEKADSSNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIER 1138 GLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTA 1079 1096 TRPRALPGVRGHIGAPMPGDVLELKIKEGDKVIKKQPLFVLSAMKMEMVIDSPIAGTVKA 1155 267 EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 387 GRAG-GVVEAAIAYTGDVIDKSRDKYDLKYYLNLADQLVKAQAHILSIKDMAGVLKPEAA 748 TAAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKL 207 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 327 561 621 629 742 TKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSA 800 913 DPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRS--EGKAPLTEVPEE 970 801 IVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPIGR~~VYRHEIPGGQLS 858 DRAD-----DLSFPKSVVDFMQGNVGQPPYGFPEPLRTKVLRGKPKVDGR-----PGE 976 QAAIEAGVQVVPGTPGPITTADEAVEFAKQYGTPIILKAAYGGGGRGIRRVDKLEEVEEA ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRIGEVVHLYERDCSLQRRHQKVVE YRSPGGAGVRLDGAAQLGGE-ITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVA TNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKP-----HGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTFRDA 512 ATDLKPAVVSPPIPYIP--AGAKPPIGLRDVLVQRGPIEFAKEVRSRPGCMITDITFRDA HOSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREA LETINTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAV 622 MPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDAV 1037 GLEIABEVDVEIESGKT-LAIQLLAEGKLNKRGEREVFFDLNGOMRSIFVVDKEASKEIV 859 NLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAG---1139 VVVPAATKVEGGDLIVVV 1156 562 208 328 388 392 452 682 069 332 447 1020

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Q7 Db g

64 G G G

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Pp

QY Db

δy

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oy Db

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A; Molecule type: DNA
A; Residues: 1-461, 'G', 463-492,'D', 494-594,'A', 596-618,'Q', 620-663,'S', 665-771,'R',773
A; Cross-references: EMBL: JOS89; NID: 9172101; PIDN: AAA34843.1; PID: 9172102
R; Morris, C.P.; Lim, F.; Mallace, J.C.
Biochem. Biophys. Res. Commun. 145, 390-396, 1987
A; Title: Yeast pyruvate carboxylase: gene isolation.
A; Reference number: S05760; MUID: 87241529; PMID: 3036126
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A:Genetics:
A:Gene
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                      cerevisiae)
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pyruvate carboxylase (EC 6.4.1.1) 1 [validated] - yeast (Saccharomyces cerew NyAlternate names: protein G3428; protein YGL062w; pyruvic carboxylase C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevision C;Pace: 31-Dec-1991 #sequence_revision 19-Jul-1996 #text_change 01-Feb-2002 C;Accession: S64066; A29233; S05760; A29722 R;Feurramn, M.; Potier, S.; Souciet, J.L. Submitted to the Protein Sequence Database, May 1996 A;Reference number: S64044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 KILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEG -- SPVKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVE
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                                                                                                                                                                                                                                                                                                                                               A.Accession: $64066
A.Molecule type: DNA
A.Residues: 1-1178 cFED.
A.Cross-references: EMBL:272584; NID:g1322565; PIDN:CAA96765.1; PID:g
A.Experimental source: strain $288C
A.Experimental source: strain $288C
J. Biol. Chem. 263, 11493-11497, 1988
A.Fitle: Sequence and domain structure of yeast pyruvate carboxylase.
A.Reference number: A92662: MUID:88298805; PMID:3042770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
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46.6%; Pred. No. 3.6e-127;
iive 175; Mismatches 400;
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A; Residues: 1003-1178 <MOR>
A; Cross-references: EMBL:J03889
A; Accession: A29722
A; Molecule type: protein
A; Residues: 1124-1149 <MOR2>
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972 QAHLDADDSKERRNSLNRL-----LFPKPTEEFLEHRRRFGNTSALDDREFFY 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1020 GLVEGRETLIRLPDVRTPLLVRLDAISEPDDK-GMRNVVANVGQIRPMRVRDRSVESVT 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 YRSPGGAGVRLDGA-AQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVA 446
                                                 447 INIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVN----KP 502
                                                                                                             441 TNIPELLILLINPVFIEGTYWTFIDDTPQLFQMVSSQNRAQKLLHYLADVAVNGSSIKG 500
321 BEITGIDIVAAQIQIAAGASLPQLGLFQDKITTRGFAIQCRITTEDPAKNFQPDTGRIEV 380
                                                                                                                                               503 HGVRPKDVAAPIDKLPNIKDL------PLPRGSRDRLKQLGPAAFARDLREQDALA 552
                                                                                                                                                                      501 QIGLPKLKSNP--SVPHLHDAQGNVINVTKSAPPSGWRQVLLEKGPAEFARQVRQFNGTL 558
                                                                                                                                                                                                                612
                                                                                                                                                                                                                            DRLDELREAMPNVNIQMLLRGRNIVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVS 672
                                                                                                                                                                                                                                                                                   673 OMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILATKDM 732
                                                                                                                                                                                                                                                                                                                                              733 AGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGOLATYFAAAQAGADAVDGASAPLSG 791
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Search completed: September 24, 2003, 16:00:27 Job time: 40.259 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 24, 2003, 15:44:03; Search time 18.6369 Seconds (without alignments) 2919.469 Million cell updates/sec Run on:

US-09-974-973A-2 5865 1 MTAITLGGILLKGIITLVST.....RVVVPAATKVEGGDLIVVVS 1157 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	crip	u [unoum oum 009300			P11154 saccharomyc			-	Q06862 anabaena sp	archaeogl				_	P37798 pseudomonas		_	_				P05165 homo sapien				P32528 saccharomyc	027179 methanobact	Q03030 salmonella	P13187 klebsiella	~	29 gallı	35 homo sa	9tts3 bos .	Q28559 ovis aries
SUMMARIES	ID	PYC_MOUSE	PYC RAT	PYC_HUMAN	PYC1_YEAST	PYC2_YEAST	PYC_PICPA	PYCA_METJA	ACCC_ANASP	PYCA_ARCFU	PYCA_METTH	ACCC_HAEIN	ACCC_ECOLI	ACCC_ECO57	ACCC_PSEAE	MCCA_HUMAN	MCCA_MOUSE	BCCA_MYCTU	ACCC_BACSU	PYCB_METJA	BCCA_MYCLE	PCCA_HUMAN	MCCA_SOYBN	MCCA_ARATH	PCCA_RAT	DUR1_YEAST	PYCB_METTH	- 1	- 1	COA1_RAT	- 1	- 1		COA1_SHEEP
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saccharomyc	~~	Saccharomyc	schizosacch	archaeoglob	methanobact	vibrio vuln	escherichia	thermotoga	vibrio para	escherichia	salmonella
P32874	000763	000955	P78820	028994	027077	08dem2	08xa38	09wz27	087sf3	P00968	P14846
HFA1_YEAST	COA2_HUMAN	COAC YEAST	COAC_SCHPO	CARB_ARCFU	CARB_METTH	CARB_VIBVU	CARB_ECO57	CARB THEMA	CARB_VIBPA	CARB_ECOLI	CARB_SALTY
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2273	2483	2233	2280	1076	1060	1077	1072	1099	1077	1072	1074
7.6	9.6	9.3	8.8	4.6	4.5	4.4	4.3	4,3	4.3	4.3	4.2
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570.5	560.5	547	5	267		25		25	25		24

ALIGNMENTS

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PLRTRAL-----EGRSEGKAPLTEVPEEEQAHLDA-DDSKERRNSLNRLLFPKPTEEFL 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGOLRSILVKDTQAMKEMHFHPKALKDVKGQIGAPMPGKVIDIKVAAGDKVAKGQPLCVL 1140
                                                                                                                                                                                                                                                                                                                                                                                                                      962 PFRSKVLKDLPRIEGRPGASLPPLNLKELEKDLIDRHGEEVTPEDVLSAAMYPDVFAQFK 1021
                                                                                                                                                                                                                                                                                                           GRPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPE 947
                                                                                                                                                                                                                                                                                                                                      GDLIKVIPSSKIVGDLAQFMVQNGLSRAEARAQAEELSFPRSVVEFLQGYIGIPHGGFPE 961
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-!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)
AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.
-!- CATALYTIC ACTIVITY: ATP + PYRUVATE + HCO(3)(-) = ADP + phosphate +
                                 651 VKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLD
                                                                                     711 YYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLA
                                                                                                        770 TYFAAAQAGADAVDGASAPLSGTTSQPSLSALVAAFAHTRRDTGLSLEAVSDLEPYWEAV
                                                                                                                                                                                RGLYLPFESGTPGPTGR--VYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEML
                                                                                                                                                                                                                                                              842 RGLYAAFDCTATMKSGNSDVYENEIPGGQYTNLHFQAHSMGLGSKFKEVKKAYVEANQML
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1001 EHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 6.4.1.1) (Pyruvic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.A., Moran S.M., Macdonald M.J.; sequence of the rat pyruvate carboxylase-encoding cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jitrapakdee S., Booker G.W., Cassady A.I., Wallace J.C.; "Cloning, sequencing and expression of rat liver pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVV 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAMKMETVVTSPMEGTIRKVHVTKDMTLEGDDLILEI 1177
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01-007-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Pyruvate carboxylase, mitochondrial precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Wistar; TISSUE-Liver;
MEDLINE-96257760; PubMed-8687410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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P52873; 064555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQL-GGEITAHF 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRPKDVA-APID-KLPNIKDLPLPRGSR 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLLLKGIITLVSTHTSSTLPA------FKKILVANRGEIAVRAFRAALETGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVAVYSEQDTGQMHRQKADEAYLIGRGLAPVQAYLHIPDIIKVAKENGVDAVHPGYGFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 FSNTFGFPIIFKAAYGGGGRGMRVVHSYEELEENYTRAYSEALAAFGNGALFVEKFIEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHIEVQILGDQYGNILHLYERDCSLQRRHQKVVEIAPATHLDPQLRSRLTSDSVKLAKQV
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                                                                                                                                                                                                                                                                                               BIOTIN CARBOXYLASE (BY SIMILARITY)
CARBOXYLTRANSFERASE (BY SIMILARITY
BIOTIN CARBOXYL CARRIER PROTEIN
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 192; Mismatches 407; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                BIOTIN (BY SIMILARITY).
W: 14CEA0F9DA8B8127 CRC64;
                                                                                                                                                                                                                                           Lipid synthesis; Transit pe
MITOCHONDRION (POTENTIAL).
PYRUVATE CARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                         P (BY SIMILARITY). SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 9e-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.5%; Score 2550.5;
                                                                                                                                                                 Pfam; PF02436; PYC_OADA; 1.
TIGRFAMS; TIGR01235; pyruv_carbox;
PROSITE; PS00188; BIOTIN; 1.
                                                    IPR005930; Pyruv_carbox.
                                                                     Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF007786; CPSase_L_D2; 1.
Pfam; PF00582; HMGL-like; 1.
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BY S
   CPase_L_N.
HMGL-like.
                                          IPR003379; PYC_OADA.
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IPR005481; C
IPR000891; B
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                                      InterPro;
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BINDING
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                                                                                                                                                                                                                           DSMLVKMICRGSDFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIG 472
                                                            GYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           770 TYFAAAQAGADAYDGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAV 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 782 AMLACAQAGADVVDVAVDSMSGMTSQPSMGALVACTKGTPLDTEVPLERVFDYSEYWEGA 841
                                                                                 DHPHLLQAPPADDEQGRILDYLADVIVNKPHGVRPKDVA-APIDKL-PNIKDLPLPRGSR
                                                                                                                                                                                                                                                                                                                                    423 DSLLVKVIAHGKDHPTAATKMSRALAEFRVRGVKTNIPFLQNVLNNQQFLAGIVDTQFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 VKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        888 GRPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPE
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P1498; Q16705;
01-0CT-1999 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVV 1156
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 ENAQLARECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVL-AESTPSKNIDDIVK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 QHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GGLLLKGIITLVSTHTSSTLPA------FKKILVANRGEIAVRAFRAALETGAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLRLLGV-----RRSSTAPVASPNVRRLEYKPIKKVMVANRGEIAIRVFRACTELGIR 62
      COFACTOR: BIOTIN AND MANGANESE (BY SIMILARITY).
PATHWAY: GIUCONEOGENESIS AND LIPOGENESIS.
SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Mitochondrial matrix.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 SAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLATEASREAEAAFGDGSVYVERAVINP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PP02785; Biotin_carb_C; 1.
Pfam; PP02785; Biotin_lipoyl; 1.
Pfam; PP00364; biotin_lipoyl; 1.
Pfam; PP00368; Crbase_L_chain; 1.
Pfam; PF02786; Crbase_L_chain; 1.
Pfam; PF02786; Crbase_L_chain; 1.
Pfam; PF02786; Pfac. Oaba; 1.
Pfam; PF00188; BIOTIN; 1.
PROSITE; PS00188; BIOTIN; 1.
Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis; ArP-binding; Mitochondrion; Lipid synthesis; Translatt peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 PYRUVATE CARBOXYLASE.

1178 PYRUVATE CARBOXYLASE.
1549 BIOTIN CARBOXYLASE (BY SIMILARITY).
1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
1178 (BY SIMILARITY).
203 ATP (BY SIMILARITY).
328 BY SIMILARITY).
1144 BIOTIN (BY SIMILARITY).
222 P -> S (IN REF. 2).
865 D -> I (IN REF. 2).
866 D -> I (IN REF. 2).
866 D -> I (IN REF. 2).
877 G -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.2%; Score 2534.5; DB 1; Length 1178; 46.2%; Pred, No. 6.3e-126;
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Conservative 188; Mismatches 409;
                                                                                                                                                                                                                                                                                                                                                                                                 IPR001882; Biotin_attach.
IPR005482; Biotin_carb_C.
IPR000089; Biotin_lipoyl.
IPR005479; CPase_L_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR005481, CPase_L_N.
IPR000891, HMGL-like.
IPR003379; PYC_OADA.
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1000
1178
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HSSP; P24182; 1BNC.
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Hum. Genet. 62:1312-1319(1998)

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SEQUENCE OF 1083-1178 FROM N.A.
MEDLINE-87212051; PubMed-3555348;
Lamhonwah A.-M., Quan F., Gravel R.A.;
Lamhonwah A.-M., around the biotin-binding site of human propionyl-
CoA carboxylase and pyruvate carboxylase.";
Arch. Biochem. Biophys. 254:631-636(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85030380; PubMed-6548474; Freytag S.O., Collier K.J.; "Molecular cloning of a cDNA for human pyruvate carboxylase." Structural relationship to other biotin-containing carboxylases and regulation of mRNA content in differentiating preadipocytes."; J. Biol. Chem. 259:12831-12837(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98254451; PubMed-9585612;
Carbone M.A., MacKay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,
Feigenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,
Seargeant L., Robinson B.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Amerindian pyruvate carboxylase deficiency is associated with two
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                            SEQUENCE FROM N.A.
TISSUB-Kidney, and Liver;
MEDILINE-8002202. PubMed-7918683;
Wexler I.D., Du Y., Lisgaris M.V., Mandal S.K., Freytag S.O., Yang B.-S., Liu T.-C., Kwon M., Patel M.S., Kerr D.S.;
"Primary amino acid sequence and structure of human pyruvate carboxylase.";
                                                                                                                                                                                                                                                                                                       TISSUE=Kidney, and Liver;
Walker M.E., Jitrapakdee S., Val D.L., Wallace J.C.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       MEDLINE=94324922, PubMed=8048912;
Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B
"cDNA cloning of human kidney pyruvate carboxylase.";
Biochem. Biophys. Res. Commun. 202:1009-1014(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS PC DEFICIENCY THR-610 AND ILE-743.
                                                                                                                                                                        Biochim. Biophys. Acta 1227:46-52(1994).
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1135-1178 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    distinct missense mutations.";
            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                TISSUE=Kidney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                 VARIANTS PC DEFICIENCY ALA-145 AND CYS-451.
MEDLINE=98244401; PubMed=9555002;
Wexler I.D., Kerr D.S., Du Y., Kaung M.M., Stephenson W., Lusk M.M.,
Wappner R.S., Higgins J.J.,
"Molecular characterization of pyruvate carboxylase deficiency in two
                                                                                                                                                     PEDIATE. RES. 43:579-584 (1998).

-!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,

INVOLVING THE AIP-DEPENDENT CARBOXYLATION OF THE COVALENTLY

AITACHED BIOTHIN THE FIRST STEP AND THE TRANSFER OF THE

CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)

AND LIPPLO (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.

-!- CATALYTIC ACTIVITY: AIP + PYIUVATE + HCO(3)(-) = ADP + Phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: Defects in PC are the cause of pyruvate carboxylase deficiency (PC deficiency) [MIM:266150] leading to lactic acidosis, mental retardation and death. It occurs in three forms: mild or type A, severe neonatal or type B, and a very mild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGRO1235; pyruv_carbox; 1.
PROSTEE; PSO0188; BIOINI; 1.
Ligase: Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (POTENTIAL).
PYRUVATE CARBOXYLASE.
BIOTIN CARBOXYLASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005524; F:ATP binding activity; TAS.
GO; GO:0009374; F:biotin binding activity; TAS.
GO; GO:0004736; F:biotin binding activity; TAS.
GO; GO:0004736; F:pyruvate carboxylase activity; TAS.
InterPro; IPRO01882; Biotin_atrach.
InterPro; IPRO05482; Biotin_lipoyl.
InterPro; IPRO05482; Biotin_lipoyl.
InterPro; IPRO05481; Cases_LD2.
InterPro; IPRO05481; Cases_LD2.
InterPro; IPRO0891; HMGL-like.
InterPro; IPRO0891; PYLOLOADA.
InterPro; IPRO05379; PYLOLOADA.
InterPro; IPRO05379; PYLOLOADA.
PFam; PF02785; Biotin_carbC; 1.
Pfam; PF00364; biotin_lipoyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                                       COFACTOR: BIOTIN AND MANGANESE.
PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00289; CPSase_L_chain;
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, U04641; AAA99537.1; -. BEMBL, S72370; AAB31500.1; -. EMBL, U30891; AA842937.1; -. EMBL; BC011617; AAH11617.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; MZ6122; AAA36423.1; -. EMBL; KO2282; AAA60033.1; -. PIR; G01933; JC2460. HSSP; P24182; IBNC. Genew; HGNC:8636; PC.
                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Homotetramer.
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                                                                                                                                          consanguineous families.
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GK; P11498; -.
MIM; 266150;
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Db 663 CEVAKENGMDVFRVFDSLNYLPNMLLGMEAAGSAG-GVVEAALSYTGDVADPSRTKYSLQ 721 Qy 711 YYLKMAEELVKSGAHILAIKDMAGLLRPAAVTKLYTALRREF-DLPVHVHTHDTAGGOLA 769 1	OY 1061 MGOIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAII 1119	PYCL_TRAST ID 01-0T-1989 (Rel. 11, Created) ID 01-0T-1996 (Rel. 34, Last sequence update) ID 01-0CT-1996 (Rel. 34, Last sequence update) IN 02 (Rel. 34, Last sequence upd
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY). FT ACT_SITE 328 203 APP (BY SIMILARITY). FT ACT_SITE 328 328 BY SIMILARITY). FT ACT_SITE 328 328 BY SIMILARITY). FT ACT_SITE 328 328 BY SIMILARITY). FT WARIANT 451 44 1144 BIOTIN (BY SIMILARITY). FT VARIANT 451 451 V-> C (in PC deficiency; mild). FT VARIANT 610 610 A-> C (in PC deficiency; mild). FT VARIANT 743 743 M-> C (in PC deficiency; mild). FT VARIANT 743 743 M-> C (in PC deficiency; mild). FT CONFLICT 352 352 A-> C (in PC deficiency; mild). FT CONFLICT 352 352 A-> C (in PC deficiency; mild). FT CONFLICT 352 352 A-> C (in PC deficiency; mild). FT CONFLICT 385 386 RS-> PT (IN REF. 2). FT CONFLICT 528 526 LA-> WP (IN REF. 2). FT CONFLICT 529 729 M-> C (in REF. 2). FT CONFLICT 638 638 B-> PT (IN REF. 2). FT CONFLICT 729 729 729 M-> A (IN REF. 2). FT CONFLICT 724 46 487 B-> R (IN REF. 2). FT CONFLICT 724 46.087 P-> A (IN REF. 2). FT CONFLICT 724 46.087 P-> A (IN REF. 2). FT CONFLICT 724 46.087 P-> A (IN REF. 2). FT CONFLICT 724 A6.087 P-> A (IN REF. 2). FT CONFLICT 725 A6.087 P-> A (IN REF. 2). FT CONFLICT 724 A6.087 P-> A (IN REF. 2). FT CONFLICT 725 A6.087 P-> A (IN REF. 2). FT CONFLICT	7 GGLLLKGIITLVSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAA 5	09 115 ENACLARECAENGITICOTPEVIDLICOKSRAVTAAKKAGIPVL-AESTPEKNIDDIVK 173

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972 QAHLDADDSKERRNSLNRL------LEPKPIEEFLEHRRRFGNISALDDREFFY 1019
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                                                                                                                                                                                                    1079 ATAEKADSSNKGHVAAPFAGV-VTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIE 1137
                                                                                                                        EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 387
                                                                                                                                                                                                                                                                       441 INIPPLITLITURVFIEGTYWTTFIDDTPQLFQMVSSQNRAQKLLHYLADVAVNGSSIKG 500
                                                                                                                                                                                                                                                                                                                         503 HGVRPKDVAAPIDKLPNIKDL-----PLPRGSRDRLKQLGPAAFARDLREQDALA 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613 DRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVS 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      792 TISQPSLSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGIPGPIGRVYRHE 851
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VAPAKTLPREVRDAILTDAVKLAKECGYRNAGTAEFLVDNQNRHYFIEINPRIQVEHTIT
                                                                                                                                          208 ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVE
                                                              IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT
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ID PYC2_YEAST
AC P32327;
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 TAAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEG--SPVKAY 88
                                                          SUBDNIT: Homotetramer.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: WITH OTHER ELOTIN CARBOXXLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Gaps
 CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 T -> G (IN REF. 1).
493 V -> D (IN REF. 1).
595 R -> A (IN REF. 1).
619 E -> O (IN REF. 1).
664 G -> S (IN REF. 1).
772 A -> R (IN REF. 1).
772 A -> R (IN REF. 1).
909 Q -> K (IN REF. 1).
130099 WW, BC7110ABAFB23E04 CRC64;
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                                                                                                                                                                                                                                                                                                                           GO; GO:0005829; C:cytosol; IDA.
GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BIOTIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 175; Mismatches 400;
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BY SIMILADT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfan, PFC2436; PYC_OADA; 1.
TIGREAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003379; PrC_OADA.
InterPro; IPR005390; Pyruv_carbox.
Pfam; PF02785; Biotin_carb C. 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00286; CPSase_L_D2; 1.
Pfam; PF00682; HMGL-like; 1.
                                                                                                                                                                                                                                                                                                                                                                     IPR005482; Biotin_carb_C. IPR000089; Biotin_lipoyl. IPR005479; CPase_L_D2.
                                                                                                                                                                                                                                                                                                                                                         IPR001882; Biotin_attach
                                                                                                                                                                                                                                                                                                                                                                                                                 IPR005481; CPase_L_N.
IPR000891; HMGL-like.
              oxaloacetate.
COFACTOR: BIOTIN AND ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
                                           PATHWAY: Gluconeogenesis.
                                                                                                                                                                                                                                                    EMBL; J03889; AAA34843.1; -. EMBL; Z72584; CAA96765.1; -.
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NP_BIND 182 187
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                                                                                                                                                                                                                                                                                 S64066; QYBYP
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- INDUCTION: By glucose.
-!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
01-0CT-1993 (Rel. 27, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FBB-203 (Rel. 41, Last annotation update)
28-FBB-203 (Rel. 41, Last annotation update)
PYLUVATE CATDOXYLASE 2 (EC 6.4.1.1) (Pyruvic carboxylase 2) (PCB 2).
PYC2 OR YBR218C OR YBR1507
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphism of the yeast pyruvate carboxylase 2 gene and protein:
                                                                                                                                                                               Stucka R., Dequin S., Salmon J.-M., Gancedo C.;
"DNA sequences in chromosomes II and VII code for pyruvate
carboxylase isoenzymes in Saccharomyces cerevisiae: analysis of
pyruvate carboxylase-deficient strains.";
Mol. Gen. Genet. 229:307-315(1991).
                                                                                                                                                                                                                                                                                                Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard Scherens B., Vierendeels F.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              effects on protein biotinylation.";
Biochem. J. 312.817-825(1995).
-!- FUNCTION: PYRUVATE CARBOXYLAGE CATALYZES A 2-STEP REACTION,
INVOLVING THE ATP-DEPRNDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
CARBOXYL GROUP TO PYRUVATE IN THE SECOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005829; C:cytosol; IDA.
GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
                                                                                                        Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96128067; PubMed~8554526;
Val D.L., Chapman-Smith A., Walker M.E., Cronan J.E.
Wallace J.C.;
                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: Gluconeogenesis.
-i- SUBUNIT: Homotetramer.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
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InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR005479; CPase_L_D2.
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InterPro; IPR005930; Pyruv_carbox.
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PF00364; biotin_lipoyl; 1.
PF00289; CPSase_L_chain; 1.
PF02786; CPSase_L_D2; 1.
                                                                                                                                                                  MEDLINE=92017667; PubMed=1921979;
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SGD; S0000422; PYC2
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                                                                                                                       NCBI_TaxID=4932;
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Pfam;
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                                                               TIGREAMS; TIGRO1235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
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AD60DA3A60F5E001 CRC64;
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S -> C (IN REE. ...
D -> E (IN REF. 1).
N -> E (IN REF. 1).
L -> F (IN REF. 1).
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N -> T (IN REF. 1).
S -> C (IN REF. 1).
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REF. 1).
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Pred. No. 9.6e-121;
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BIOTIN (BY 5
Pfam; PF00682; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSVESVTATAEKADSSNKGHVAAPFAGV-VTVTVAEGDEVKAGDAVAIJEAMKMEATITA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LFPKPIEEFLEHRRFGNTSAL 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDK-GMRNVVANVNGQIRPMRVRD 1071
                                                                                                                                                                                                                                                                                                                                                                                       964
                                           850 PEVYQHEIPGGQLTNLLFQAQQLGLGEQWAETKRAYREANYLLGDIVKVTPTSKVVGDLA 909
              DALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAH 725
                                                                                                     ILAIKDMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDG 784
                                                                                                                                                                                                                            Yeast 14:647-654(1998).
-!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTHN IN THE FIRST STEP AND THE TRANSFER OF THE
CARBOXYL GROUP TO PYRUVATE IN THE SECOND (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + PYFUVATE + HCO(3)(-) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                             ASAPLSGITSQPSLSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPT
                                                                                                                                                                                                                                                                                                                                                                                905 LHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPL
                                                                                                                                                                                                                                                                                      845 GRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE=98301182; PubMed=96393111;
Menendez J., Delgado J., Gancedo C.;
"Isolation of the Pichia pastoris PYC1 gene encoding prarboxylase and identification of a suppressor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1189 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVDGKIERVVVPAATKVEGGDLIVVV 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1144 PADGQVKDVFIKDGESVDASDLLVVL 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            965 TEVPEEEQAHLDADDSKERRNSLNRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: BIOTIN AND ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: Gluconeogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pichia pastoris (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYC_PICPA
P78992;
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                                                       673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 VGDKVSARNLAYAANVPTV-PGTPGP-IEDVAQATAFVEEYGYPVIIKAAFGGGGRGMRV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLAD 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVEFRIRGVKTNIPFLLALLTHPVFMTSECWTTFIDDTPELFKILTSQNRAQKLLAYLGD 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KPHGVRPKDVAAPIDKLPNIKD--LPLPRGSRDRLKQLGPAAFAR 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGDKSRAVTAAKKAGLPVLAESTPSKNIDDIVKS---AEGQTYPIFVKAVAGGGGRGMRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSSPDELRKLATEASREAEAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRPDTGTITAYRSPGGAGVRLDGAAQLGGE-ITAHFDSMLVKMTCRGSDFETAVARAQRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
BY SIMILARITY.
BIOTIN (BY SIMILARITY).
WW: BBGE858079657914 CRC64;
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1.8e-118;
thes 419;
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                                                                                                                                                                           InterPro: IPR001883; Biotin_attach.
InterPro: IPR005483; Biotin_carb_C.
InterPro: IPR000089; Biotin_lipoyl.
InterPro: IPR005483; CPase_L.
InterPro: IPR005493; CPase_L.D2.
InterPro: IPR005491; GPase_L.D2.
InterPro: IPR005641; GPase_L.D2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGREAMS; TIGR01235; pyruv_carbox; PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003379; PYC_OADA.
InterPro; IPR005930; Pyruv_carbox.
Pfam; PF02785; Biotin_arb_C; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1189 AA; 131400 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF02786; CPSase_L_D2; 1.
PF00682; HMGL-like; 1.
PF02436; PYC_OADA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00866; CPSASE_1; 1. PROSITE; PS00867; CPSASE_2; 1.
                                                                                                                                     EMBL; Y11106; CAA71993.1; -. HSSP; P24182; 1DV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190
315
1140
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les 529; Conserv
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
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Matches
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960 GKAPLTEVPEEEQA---HLDADDSKERRNSL-NRLLFPKPTEEFLEHRRRFGNTSALDDR 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1016 EFFY -- GLVEGRETLIRLPDVRTPLLVRLDAISE-PDDKGMRNVVANVNGQIRPMRVRDR 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1029 NFLSPPKIDEERHYTIVTIETRKTLIIKCMAEGELSOSSGTREVYFELNGEMRKVTVEDK 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1073 SVESVTATAEKADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITAS 1131
                                                                      MRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFR 663
                                                                                                                                               724 AHILAIKDMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAV 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494 LAVNGSSIKGQIGLPKLH--KEADIPSITDINGDVIDVSIPPPDGWRQFLLEKGPEQFAQ 551
                                        DLREQDALAVIDTTFRDAHQSLLATRVRSFALKPAAEAVAKLJPELLSVEAWGGATYDVA 603
                                                                                                                                                                                                                                                                                                                            730 THILAVKDMAGTLKPTAAKQLISALRRKFPSLPIHVHTHDSAGTGVASMVACARAGADVV 789
                                                                                                                                                                                                                                                                                                                                                                     783 DGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPG 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGD 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSE--- 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          909 LAQFMVSNKLSSEDVERLASELDFPDSVLDFFEGLMGTPYGGFPEPLRTNVISGKRRKLT 968
                                                                                                                                                                                                       664 IFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAIN-JAL-1 / DSM 2661 / ATCC 43067;

WEDLINE-9637999; PubMed-868087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Button G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1132 VDGKIERVVVPAATKVEGGDLI 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAGRIGOIAVKENDSVDASDLI 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2190;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNIDAILNVAEKAKVDAIHPGYGFLAENAEFARAVKKAGFEFIGPNPDAIEAMGSKINAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 TAAKKAGLPVLAESTPS-KNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
                                                                                                                                                              FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND.
                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IS 80-90 DEGREES CELSIUS.
-:- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
                                                                                                                                                                                                                                                                                                                      CONCENTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 KIMKKAGVPLIPGSEGAIEDIDEAIEIAEAIGFPVVVKASAGGGGMGMSVAYSKEELKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 FKKILVANRGELAVRAFRAALETGAATVALYPREDRGSFHRSFASEAVRIGTEGSPVKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FNKVLIANRGELAIRIIRACWELGIKTVAVYSEADKRSLHATLADEAYCIG-PAPAAKSY
                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: Gluconeogenesis.
SUBURIT: HETEROCOTAMER OF FOUR A AND FOUR B SUBUNITS.
MASS SPECTROMETRY: MW-55500; METHOD-MALDI.
MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
                                                                                                                                                                                                                                                                                                                      BY MAGNESIUM, WHEN ITS CONCENTRATION HIGH CONCENTRATION OF ATP AND ALPHA-
                                                                                                                                                                                                                                                                                 -!- COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
                                                               MEDLINE-21034791; PubMed-11195096; Mukhopadhyay B., Patel V.J., Wolfe R.S.; A stable archaeal pyruvate carboxylase from the hyperthermophile Methanococus jannaschii."; Arch. Microbiol. 174:406-414(2000).
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04D2E401892F872F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%; Score 1079; DB 1; 48.0%; Pred. No. 8.5e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR004549; Accc.
InterPro, IPR005482; Biotin_carb_C.
InterPro, IPR005483; CPase_L.
                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION: INHIBITED EXCEEDED THE ATP ONE, AND BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR005479; CPase_L_D2.
InterPro, IPR005481; CPase_L_N.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00289; CPase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85;
                                                     SEQUENCE OF 1-12, AND FUNCTION MEDLINE-21034791; Pubmed-11195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
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TIGREAMS; TIGR00514; accC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U67563; AAB99232.1; -. PIR; D64453; D64453.
jannaschii.";
Science 273:1058-1073(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P24182; 1BNC.
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                                                                                                                                                                                                                                                                                                                                                            KETOGLUTARATE.
                                                                                                                                                                                                                                                                 oxaloacetate.
                                                                                                                                                                                                                                                                                                     BICARBONATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217;
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                           ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRIGEVVHLYERDCSLQRRHQKVVE 267
                                                                   268 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 327
                                                                                               241 EAPSPIMTEELRERMGEAAIKAGKAINYDSAGTVEFLY-ENGNFYFLEMNTRIQVEHTVT 299
                                                                                                                              EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLASE CATALYZES THE CARBOXYLASE CATALYZES THE CARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.

CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2) PATHWAY: Long-chain fatty acid biosynthesis; first step.

SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
                                                                                                                                                                                       388 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX. SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gornicki P., Scappino L.A., Haselkorn R.; "Genes for two subunits of acetyl coenzyme A carboxylase of Anabaena sp. strain PCC 7120: biotin carboxylase and biotin carboxyl carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCC OR ALRÓ939.
Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                            acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biotin carboxylase (EC 6.3.4.14) (A subunit of carboxylase) (EC 6.4.1.2) (ACC).
                                                                                                                                                                                                                                                                         NIGFLRALLREEDFTSKRIATGFIGDHPHLLQ 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 175:5268-5272(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93352435; PubMed=8102363;
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                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                            ACCC_ANASP
Q06862;
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                                                                                                                                                                                                                                                                                 417
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ETMOKAGVPTVPGSEGLVETEQEGLE----LAKDIGYPVMIKATAGGGGRGMRLVRSPDE 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 KLLEEAPSPALDSDLREKMGQAAVKAAQFINYTGAGTIEFLLDRSGQFYFMEMNTRIQVE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 TITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVS 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 TAAKKAGLPVLAES----TPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDE
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PYCA OR AF0220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.6%; Score 1032.5; DB 1; Lengun
48.2%; Pred. No. 2e-47;
... v.:matrhes 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
8A541B38B39E00F9 CRC64;
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PROSITE; PS00867; CPSASE_2; 1.
Fatty acid biosynthesis; Ligase; Biotin; ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             506 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVATNIGFLRALLREEDFTSKRIATGFI 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: | || | : : | GLPTIGFHQRIMENPQFLQGNVSTSFV 442
email to license@isb-sib.ch).
                                                                                                                                                                                    InterPro; IPR004549; Accc.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005493; Orbase_L_D2.
InterPro; IPR005491; CPase_L_D2.
InterPro; IPR005481; CPase_L_N.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF02786; CPase_L_chain; 1.
Pfam; PF02786; CPase_L_chain; 1.
IIGRFAMS; TIGR00514; accC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobaceae; Archaeoglobus.
NCBL_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49104 MW;
                                                                                    BAB72896.1;
                                                          L14862; AAB51770.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaeoglobus fulgidus.
                                                                                                     PIR; A53311; A53311.
PIR; AH1923; AH1923.
HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
  send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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PYCA_MRCFU

ID PYCA_MA
AC 030019;
DT 30-MAY
DT 16-0CT-
DT PYCTOAT
DY ACTOAT
CO ATCHAGE
OC ATCHAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=187420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Delta H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N
STRAIN=Delta H;
                                                                                                                                                                                                                                                                                                                                                                             PYCA_METTH
                  121
                                                                                                      269
                                                                                                                                                              329
                                                                                                                                                                                                                                                                            449
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                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 TAAKKAGLPVLAESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                      FUNCTION: PYROVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE AIP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL CAROUT TO PYROVATE IN THE SECOND.

CATALYTIC ACTIVITY: ATP + PYTUVATE + HCO(3)(-) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
                                                                                                                              Zhou L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGRO0514; accc; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; FALSE_NEG.
Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSKILVANRGEIAVRVMRACRELGIKTVGVYSSADKRAFHRVYADECYYIG-KADPRDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                      MEDLINE-98049343; PubMed=9989475;
Klenk H.-P., Clayton R.A., Tomb J.-F., white O., Nelson K.E.,
Klenk H.-P., Clayton R.A., Tomb J.-F., white O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L
Overbeek R., Gocayne J.D., Weidman J.E., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Raine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: AIP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
39B765F319235AD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 1.1e-46; 76; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.4%; Score 1020; DB 1; 47.9%; Pred. No. 1.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
                                                                                                                                                                                                                              reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                  AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004549; Accc.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005481; CPase_L.D2.
Pfam; PF02785; Biotin_carb_C; IPR002785; Biotin_carb_C; IPR00289; CPGase_L.Chain; I
                                                                                                                                                                                                                                                                                                                                                          BICARBONATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001090; AAB91012.1; -.
PIR; D69277; D69277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Complete proteome
NP BIND 161 166 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57438 MW;
                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Gluconeogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                oxaloacetate.
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; AF0220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
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Best Local
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448
                            ESMORAGVPVIPGSPKIDTVDEAKEWAEKIGYPVAVKASGGGGGIGIVVVNSQEELEEAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI 268
                                                                                                                                                                                                                                                                       APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 328
                                                                                                                                                                                                                                                                                                                                                                                                                               EVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNGFRPDTGIITAY 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND. THE MAXIMUM ACTIVITY IS AT PH 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Gluconeogenesis.
SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
                                                                                                                                                                                                                                                                                                                        RKSKKLGESYFKDSTVYLEKYLARPRHIEVQILADQHGNVIHLGERECSIQRRHQKLIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 VVTGIDIVKYQIRIAYG---EELRHGQEDVAIRGHAIECRINAEDPVN-FYPRSGRILHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dubois J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND 60 DEGREES CELSIUS. CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGULATION: INHIBITED BY ADP AND ALPHA-KETOGLUTARATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98148063; PubMed=9478969; Mukhopadhyay B D. Stoddard S.P., Wolfe R.S.; Mushopadhyay B D. Stoddard S.P., Wolfe R.S.; Pubmedation, regulation, and molecular and biochemical characterization of pyruvate carboxylase from Methanobacterium thermoautotrophicum Strain deltaH."; J. Biol. Chem. 273:5155-5166(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taH: functional analysis and comparative genomics."; Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 1-17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prca OR MTH1917. Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGFLRALLREEDFTSKRIATGFI 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98037514; PubMed=9371463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKVVIANRGEIALRILRACKELGIKTVAVHSTADRDLKHVLLADETICIGPAPS-AKSYL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCIENCE 269:496-512(1995).

-I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE CAPLIZES THE CARBOXYLASE CAPLIZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: ATP + blotin-carboxyl-carrier protein + CO(2).

- ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

-I- PATHWA: Long-chain fatty acid blosynthesis; first step.

-I- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BICTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY). SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOXL-PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL
                                                                                                                                                                                                                                                     Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterpack T.K., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                              Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152; Indels
  Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
2B497E2A31ED96D1 CRC64;
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PROSITE; PS00867; CPSASE_2; 1.
Fatty acid biosynthesis; Ligase; Biotin; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 send an email to license@isb-sib.ch).
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Interpro: IPR005449; Biothin_carb_C.
Interpro: IPR005479; CPase_L_D2.
Interpro: IPR005481; CPase_L_N.
Pfam: PP02785; Biothin_carb_C; 1.
Pfam: PP02789; CPsase_L_chain; 1.
Pfam: PP02786; CPsase_L_chain; 1.
                                                                                                                                                                                                                STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                   carboxylase) [EC 6.4.1.2) (ACC) ACC OR HI0972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49108 MW;
                                                                                              Bacteria; Proteobacteria; Gamr
Pasteurellaceae; Haemophilus.
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les 212; Conservative
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                                                                     Haemophilus influenzae.
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448 AA;
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                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                          NCBI_TaxID=727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
SEQUENCE
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 KLMKKAGVPVIPGTDQGVSDPDEAARIADSIGYPVIIKASAGGGGIGMRAVYEEDELIRA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 YRSPGGIGVRVDSGVYMNYEIPPFYDSMISKLIVWGMDRQEAINRMKRALSEYIILGVKT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 TAAKKAGLPVLAESTPS-KNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRIGEVVHLYERDCSLQRRHQKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 MESTQSVAASAFGDPTVYIEKYLERPRHIEFQVMADESGNVIHLADRECSIQRRHQKLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAPSPIMTPELRERMGSAAVKAAEYIGYENAGTVEFLY - SNGDFYFLEMNTRIQVEHPIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY)
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 TIPFHKAIMRNEAFRRGELHTHFVDEY 443
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AND CARBAMYL PHOSPHATE SYNTHETASES.
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                                                                                                                                                                                                                                                                                                  InterPro; IPR004549, AccC.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005491; CPasse_L_D2.
InterPro; IPR005481; CPasse_L_N.
Pfam; PF002785; Biotin_carb_C; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS, TIGR00514, accc; 1. PROSITE, PS00866; CPSASE_1; 1. PROSITE; PS00867; CPSASE_2; 1.
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                                                                                                                                                                                                                                      EMBL; AE000942; AAB86377.1; -.
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                                                                                                                                                                                                                                                               PIR; A69123; A69123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 AA;
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                                                                                                                                                                                                                                                                                     1 BNC
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01-NOV-1995
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P43873;
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 GKVNHLHSPGGLGVRWDSHVYGGYTVPPHYDSMIAKLITYGDTREVAIRRMQNALSETII 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 EHPVTEMITGVDLVKEQLRIAAGL---PISFKQEDIKVKGHAMECRINAEDPKT-FLPSP 351
   150 AAKKAGLPVLAEST-PSKNIDDIVKS---AEGQIYPIFVKAVAGGGGRGMRFVSSPDELR
                                                                                                                                  206 KLATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKV
                                                                                                                                                                                                                                                              VEIAPAQHLDPELRDRI----CADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 EHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 GTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV
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MEDLINE-92112819; PubMed-1370469;
Li S.-J., Cronan J.E. Jr.;
"The gene encoding the biotin carboxylase subunit of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kondo H., Shiratsuchi K., Yoshimoto T., Masuda T., Kitazono A.,
Tsuru D., Anai M., Sekiguchi M., Tanabe T.;
"Acetyl-CoA carboxylase from Escherichia coli: gene organization and
nucleotide sequence of the biotin carboxylase subunit.";
Proc. Natl. Acad. Sci. U.S.A. 88:9730-9733(1991).
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SEQUENCE FROM N.A.
MEDILINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA accC OR FABG OR B3256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best E.A., Knauf V.C.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 AA.
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J. Biol. Chem. 267:855-863(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 DGIKTNIPLHELILEDENF 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 275:16183-16190(2000).

-!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE CAMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLASE CAPTILY OF THE ACREIF PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
-!- CAPALYTIC ACTIVITY: ATP + blotin-carboxyl-carrier protein.
-!- PATHWAY: Long-chain fatty acid blosynthesis; first step.
-!- PATHWAY: Long-chain fatty acid blosynthesis; first step.
-!- STBUNIT: ACRETYL-COA CARBOXYLASE IS AN HETEROHEXANDER OF BIOTIN CARBOXYL ACREDIA PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2.2 COMPLEX.
-!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOXL-
                                                                                                                                          properties of proteins encoded
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                                                                                                                                                                                                                                                                                                                                        Waldrop G.L., Rayment I., Holden H.M.;
"Three-dimensional structure of the biotin carboxylase subunit of acetyl-CoA carboxylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20283656; PubMed=10821865;
Thoden J.B., Blanchard C.Z., Holden H.M., Waldrop G.L.;
"Movement of the biotin carboxylase B-domain as a result of ATP
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CA -> SR (IN REF. 2)
L -> M (IN REF. 1).
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                                                                                             Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed pin the genome of Escherichia coli K-12. Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
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Interpro; IPR005481; Biotin_carb_C.
Interpro; IPR00549; CPase_L_D2.
Interpro; IPR005481; CPase_L_N.
Pfam; PP02785; Biotin_carb_C; I.
Pfam; PP02786; CPsase_L_Carbin; I.
Pfam; PP02786; CPsase_L_D2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 33:10249-10256(1994).
SEQUENCE OF 1-12.
STRAIN-K12 / EMG2;
MEDLINE-97443975; PubMed=9298646;
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PROSITE; PS00867; CPSASE_2;
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PDB, 1BNC; 30-AUG-95.
PDB, 1DV1; 09-JUN-00.
PDB, 1DV2; 09-JUN-00.
PDB, 1K69; 05-DEC-01.
Ecodene, EG10276; accC.
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     123 MKKAGVPCVPGSDGPLG-DDMDKNRAIAKRIGYPVIIKASGGGGGRGMRVVRGDAELAQS 181
                                                                                                                                                                                                                                                       388 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 447
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MEDLINE-21156231; PUDMed=11258796;
MEDLINE-21156231; PUDMed=11258796;
MEDLINE-21156231; PUDMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayawa K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli ol57:H7 and genomic comparison with a laboratory strain K-12.";
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-I-CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

-I-PATHMAY: Long-chain fatty acid biosynthesis; first step.

-I-PATHMAY: LONg-chain fatty acid biosynthesis; first step.

-I-SAUBUNT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS
OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (By similarity).
                                                                                                                                  242 EAPAPGIIPELRRYIGERCAKACVDIGYRGAGTFEFLF-ENGEFYFIEMNTRIQVEHPVT
                                         208 ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVE
                                                          EEVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA
                                                                                                             IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT
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STRAIN-0157:H7 'EDL933 / ATCC 700927;
PETD N. T. Plunkett G. III, Burland V. Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans D.S., Gregor J., Kirkpatrick H.A.,
Grobeck E.J., Davis N.W., Lim A., Dimalanta E.I., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Abrodens sequence of entrone Res.,
Mature 409:529-533(2001).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biotin carboxylase (EC 6.3.4.14) (A subunit of carboxylase) (EC 6.4.1.2) (ACC).
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NVDLQIRIMNDENF 430
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46.8%; Pred. No. 1.5e-42;
ive 66; Mismatches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::||| ||| : |: || : ::|||: |: || : |: || : || : || : || : || : ||: || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 IDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVTA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPAIISAAEITGAVAIHPGYGFLSENANFAEQVERSGFIFIGPKAETIRLMGDKVSAIAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 EAPAPGITPELRRYIGERCAKACVDIGYRGAGTFEFLF-ENGEFYFIEMNTRIQVEHPVT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 EEVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNGFRPDIGTITA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AKKAGLPVLAESTPSKNIDDIVKS---AEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 MKKAGVPCVPGSDGPLG-DDMDKNRAIAKRIGYPVIIKASGGGGGGGRGMRVVRGDAELAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA carboxylase) (EC 6.4.1.2) (ACC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pred. No. 1.9e-42;
66; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
BC5716323F6233ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO0514; accC; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
Fatty acid biosynthesis; Ligase; Biotin; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 1;
1.9e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.0%; Score 938; 46.8%; Pred. No. 1
                                                                                                                                                                                                                               InterPro; IPR004549; AccC.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005491; CPase_L_D2.
InterPro; IPR005491; CPase_L_N.
Fam; PF00289; CPsase_L_chain; 1.
Pfam; PF00289; CPsase_L_chain; 1.
Pfam; PF02786; CPsase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                               EMBL; AE005553; AAG58384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49337 MW;
                                                                                                                                                                                                    BAB37551.1;
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Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168
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                                                                                                                                                                                                                      PIR; H91144; H91144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 AA;
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                                                                                                                                                                                                    AP002564;
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-I FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALIZES THE CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARDOXYL GROUP TO FORM MALONYL-COA.

-I CATALITIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

-I PATHWAY: Long-chain fatty acid biosynthesis; first step.

-I DATHWAY: Long-chain fatty acid biosynthesis; first step.

-I SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARRIEX PROTEIN, BIOTIN CARBOXYLASE AND CARBOXYLASE IN A 2:2 COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 15692 / PAO1;
MEDIIAR=2043137; PubMed=10984043;
MEDIIAR=2043137; PubMed=10984043;
Stover C.K., Pham X.O.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westprock Wadman S., Yuan Y., Smrobr R.L., Goltry L., Tolentino E. Westprock Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                           STRAIN=ATCC 15692 / PAO1;
BEDLINE-24042851; PubMed=7693652;
Best E.A., Knauf V.C.;
"Organization and nucleotide sequences of the genes encoding the blotun carbboxyl carrier protein and blotin carboxylase protein of Pseudomonas aceryl coenzyme A carboxylase.";
J. Bacteriol. 175:6881-6889(1993).
                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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PROSITE; PS00867; CPSASE_2; 1.
Fatty acid biosynthesis; Ligase; Biotin; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005479; CPase_L_D2.
InterPro; IPR005481; CPase_L_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP
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Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
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                                                                       Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L14612; AAA16041.1; -.
EMBL; AE004898; AAC08233.1;
PIR; B49342; B49342.
HSSP; P24182; 1BNC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHATE SYNTHETASES.
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Pseudomonas aeruginosa
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                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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89

30 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL

us-09-974-973a-2.rsp

molecular cause of 3-methylcrotonyl-CoA: carboxylase

D οŽ

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242 EAPAPGIDEKARQEVFARCVQACIEIGYRGAGTFEFLY-ENGRFYFIEMNTRVQVEHPVS 300
                                                                                                                                                                                                                                                                           90 DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149
                                                     150 AAKKAGLPVL--AESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKL 207
                                                                                                                     122 AMKRAGVPTVPGSDGPLPEDEETALAIAREVGYPVIIKAAGGGGGRGMRVVYDESELIKS: 181
                                                                                                                                                 208 ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVE 267
                                                                                                                                                                          182 AKLTRTEAGAAFGNPMYYLEKFLTNPRHVEVQVLSDGQGNAIHLGDRDCSLQRRHQKVIE 241
                                                                                                                                                                                                    268 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 327
                                                                                                                                                                                                                                                           EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 387
                                                                                                                                                                                                                                                                                                                                          357 FHAPGGNGVRVDSHLYSGYSVPPNYDSLVGKVITYGADRDEALARMRNALDELIVDGIKT 416
           3 EKVLIANRGEIALRILRACKELGIKTVAVHSTADRELMHLSLADESVCIG-PAPATQSYL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANT HIS-464.

MEDLINE=21295033; PubMed=11401427;
Obata K., Fukuda T., Morishita R., Abe S., Asakawa S., Yamaguchi S.,
Yoshino M., Ihara K., Murayama K., Shigemoto K., Shimizu N., Kondo I.;
"Human biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase
gene (MCCA): cDNA sequence, genomic organization, localization to
chromosomal band 3q27, and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Cloning of the human MCCA and MCCB genes and mutations therein reveal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11170888;
Gallardo M.E., Desviat L.R., Rodriguez J.M., Esparza-Gordillo J.,
Perez-Cerda C., Perez B., Rodriguez-Pombo P., Criado O., Sanz R.,
Morton D.H., Gibson K.M., Le T.P., Ribes A., Rodriguez de Cordoba S.,
Ugarte M., Penalva M.A.,
"The molecular basis of 3-methylcrotonylglycinuria, a disorder of
                                                                                                                                                                                                                                                                                                                388 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              096R03; Q9H959; Q9NS97; 28-FFB-2003 (Rel. 41, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
15-SFP-2003 (Rel. 42, Last sequence update)
Methylcrotoryl-CoA carboxylase alpha chain, mitochondrial precursor (BC 6.4.1.4) (3-Methylcrotoryl-CoA carboxylase alpha subunit) (3-methylcrotoryl-CoA carboxylase 1) (MCCase alpha subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holzinger A., Roeschinger W., Lagler F., Mayerhofer P.U., Lichtner Kattenfeld T., Thuy L.P., Nyhan W.L., Koch H.G., Muntau A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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MEDINES R.D., Collins F.S., Magner L., Schemder C.M., Schuler G.D.,

MISCAPLE S., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MEDINES R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

MEDINES M., Modern K., Farmer A.A., Rubin G.M., Hong L.,

MEDINES M., McEwan P.J., McKernan K.J., Malek J.A., Gunerathe P.H.,

MEDINES S.A., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

MILIAION D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

MILITING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MILITING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MILITING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MILTING M., Madan J.W., Green E.D., Dickson M.C.,

MILTAIGH Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Mediquez A.C., Grimwood J., Schmutz J., Myers R.M.,

Mutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Meneration and initial analysis of more than 15,000 full-length

MEDINES M. Madan J. S., Morelled W.S.,

Meneration and initial analysis of more than 15,000 full-length

Meneration and initial analysis of more than 15,000 full-length

MEDINES M. M. Madan J. S., Marphyller, D. March J. Shorth J. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Naganari K., Masuho Y., Sasaki N.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: Leucine catabolism.
-i- SUBNUT: Probably a dodecamer composed of six biotin-containing alpha subunits and six beta subunits.
-i- SUBNUT: ALCATION: Mitochondrial matrix.
-i- DISEASE: Defects in MCCC1 are the cause of 3-
methylcrotonylglycinuria type I (MCGI) [MIM:210200]; also designated CGA or CG2. MCGI is a recessive disease that is characterized by muscular hypotonia and atrophy, probably of
                                                                                                                  [4]
SEQUENCE FROM N.A., AND VARIANTS MCGI VAL-289; SER-385; PRO-437 AND
                                                                                                                                                                                                                                                                                                                          Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N.,
                                                                                                                                                                                                                                                                                                                                                                             Packman S., Baumgartner E.R., Valle D.; "The molecular basis of human 3-methylcrotonyl-CoA carboxylase
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EMBL; AB020826; BAA99407.1; --
EMBL; AB020826; BAA99407.1; --
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EMBL; AK023051; BAB1437.1;
EMBL; BC004214; AAH04214.1;
EMBL; BC004187; AAH04187.1;
Genew; HGNC:6936; MCCC1.
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deficiency.
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      R MIM; 210200; ...
R GO; GO:0005759; C:mitochondrial matrix; NAS.
R GO; GO:0004485; F:methyluchidning activity; NAS.
R GO; GO:0004485; F:methylucrotonyl-coA carboxylase activity; NAS.
R GO; GO:0006768; P:biotin metabolism; NAS.
R GO; GO:0006768; P:biotin metabolism; NAS.
R GO; GO:0006768; P:biotin metabolism; NAS.
R GO; GO:0006768; P:biotin_attach.
R InterPro; IPR001892; Biotin_attach.
R InterPro; IPR001893; Biotin_attach.
R InterPro; IPR00549; CPase_L_D2.
R InterPro; IPR00549; CPase_L_D2.
R InterPro; IPR00549; CPase_L_D2.
R Ffam; PF002785; Biotin_carb_C; 1.
R Ffam; PF002785; CPase_L_Chain; 1.
DR R Ffam; PF00289; CPase_L_Chain; 1.
DR ROSITE; PS00188; BIOTIN; 1.
DR RNOSITE; PS00188; BIOTIN; 1.
DR RHOSITE; PS00867; CPSASE_L; 1.
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METHYLCROTONYL-COA CARBOXYLASE ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%; Score 897; DB 1; Length 725; 36.1%; Pred. No. 5.4e-40; Live 96; Mismatches 206; Indels
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/FTId=VAR_012787.
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/FTId=VAR_012790.
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492	457 QYNIVGLPTNIDFLINLSGHPEFEAGNVHIDFIPQH		Ω
498	439 EFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVT 498		Οy
456	397 PVAGPLVHLSTPRADPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYSLR 456		QQ
438	380 PDIGIITAYRSP-GGAGVRLDGAAQLGGEIIAHFDSMLVKMTCRGSDFEIAVARAQRALA 438		ΟŸ

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_unclassified:*

sp_rodent:*

10: 111: 12: 14:

sp_plant:* sp_virus:*

sp_phage:*

sp_rvirus:* sp_bacteriap:*

sp_archeap:*

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*

SUMMARIES

	Description	Q812g4 corynebacte	054587 corynebacte	Q8frq0 corynebacte	Q8rgl2 corynebacte	Q9rk64 streptomyce	Q9f843 mycobacteri	P95127 mycobacteri	Q50450 mycobacteri	Q8jhf6 gallus gall	Q9k9m0 bacillus ha	Q9kwu4 bacillus su	Q9ddtl brachydanio	P94448 bacillus st	Q9hes8 aspergillus	Q8y846 listeria mo	Q92cw1 listeria in
	ID	Q8L2G4	054587	Q8FRQ0	Q8RQL2	Q9RK64	Q9F843	P95127	050450	Q8JHF6	Q9K9M0	Q9KWU4	Q9DDT1	P94448	Q9HES8	Q8Y846	Q92CW1
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	uery Match Length DB	1140	1140	1168	1139	1124	1127	1127	1124	1178	1150	1148	1180	1147	1192	1146	1146
æ	Query	98.4	98.2	7.06	90.3	64.7	64.6	63.3	59.4	43.5	43.2	43.1	43.0	42.8	42.8	42.5	42.5
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ALIGNMENTS

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Bacieria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterinae; Corynebacterium.
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COTYPOEDACTERING CEENALUM CD945."

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

REBE; AF503915; AAM27458.1;

RICHEPPO; IPR001882; Biotin_attach.

RICHEPPO; IPR000482; Biotin_attach.

RICHEPPO; IPR000482; Biotin_lipoyl.

RICHEPPO; IPR000481; Biotin_lipoyl.

RICHEPPO; IPR000481; CPase_L.D2.

RICHEPPO; IPR000891; HMGL-like.

RICHEPPO; IPR000891; HMGL-like.

RICHEPPO; IPR000891; PWC_OADA.

RICHEPPO; IPR005930; PYCC_OADA.

REPEAM: PF02786; Biotin_carb_c; I.

REPEAM: PF02786; Biotin_carb_c; I.

REPEAM: PF02786; Biotin_lipoyl; I.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                               PRT; 1140 AA.
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                                                                                                                                    PRELIMINARY;
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RESULT 1
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QY 1038 LLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1097 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 2 054587 ID 054587; AC 054587; PRT; 1140 AA. DT 01-JUN-1998 (TEMBLE) 06, Created) DT 01-JUN-1998 (TEMBLE) 06, Last sequence update) DT 01-MAR-2003 (TEMBLE) 05, Last sequence update)	Pyruvate carboxylase (EC 6.4.1.1) PYC OR CGL0689. Corynebacterium glutamicum (Brevi Bacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteria; Norgania; No	STRAIN-1253; KOffas M.A.G., Ramamoorthi R., Pine W.A., Sinskey A.J., Stephanopoulos G.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. [2] SEQUENCE FROM N.A. STRAIN-ATCC 13032; Defent-Wondisch D.G. Krentrer C. Kalinowski T. Datab M. Gahm.	Eikmann B.J.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. [3] SEQUENCE FROM N.A. STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025; Nakagawa S.; "Complete genomic sequence of Corynebacterium glutamicum ATC submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.	CC -!- COFACTOR: BIOTIN (BY SIMILARITY). DR EMBL; AF038484; AAB92588.1; DR EMBL; AF0365276; BAB98082.1; DR EMBL; P24182.1 LBNC. DR InterPro; IPR001882; Biotin_attach. DR InterPro; IPR005482; Biotin_attach. DR InterPro; IPR005482; Biotin_lipoyl. DR InterPro; IPR006482; Biotin_lipoyl. DR InterPro; IPR006482; Biotin_lipoyl.	Interpro; IPR005491 Interpro; IPR003379 Interpro; IPR003379 Interpro; IPR005830 Pfam; PF02785; Biot Pfam; PF00284; Biot Pfam; PF00289; CPSa Pfam; PF00682; CPSa Pfam; PF00682; HWGL Pfam; PF0488; PYC_ TICKPAMS; 11GR02436; PYC_	DR PROSITE; PS00188; BIOTIN; I. DR PROSITE; PS00188; BIOTIN; I. DR PROSITE; PS00188; BIOTIN; I. DR PROSITE; PS001867; DESASRE_2; I. KW Biotin; Ligase; Pyruvate; Complete proteome. SQ SEQUENCE 1140 AA; 123102 MM; 2A6D484ED2FEB531 CRC64; Query Match Query Match Best Local Similarity 99.4%; Pred. No. 1.7e-299; Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0; QY 18 VSTHTSSTLPAPKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVR 77
Query Match 98.4%; Score 5772; DB 2; Length 1140; Best Local Similarity 99.6%; Pred. No. 3.4e-300; Matches 1135; Conservative 4; Mismatches 1; Indels 0; Gaps 0; 18 VSTHTSSTLPAFKKILVANRGEIAVRAFRALETGAATVAIYPREDRGSFHRSFASEAVR 77 :	78 IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLGENAQIARECAENGIIFIGPTPEV 137 [11111111111111111111111111111111111	SRTGEVVHLYERDCS	318 PRIQVEHTVIEEVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNG 377	YLADV YLADV YTDTT VTDTT	8 FRDAH 1 1 1 1 1 1 1 1 1 1	678 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYILDYYLKMAEETVKSGAEILAIKDMAGIJR 737	VVGDLALHLVGAGV VVVGDLALHLVGAGV VVVGDLALHLVGAGV SEGKAPLTEVPEEEQ SEGKAPLTEVPEEEQ STGLVEGRETLIRLP

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EMBL; AP005216; BAC17519.1;
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.
Ikeo K., Suzuki M., Mashima J., Itch T., Yamaqıshi A., Nishio Usuda Y., Sugimoto S.;
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Corynebacterineae, Corynebacteriaceae, Corynebacterium
                                                     01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAR-2003
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                                                                                                                                                                                                                                                                        923 VSPEDFAADPOKYDIPDSVIAFLRGELGTPPGGWPEPLRTRALEGRSOGKAPLAEIPAEE
                                                                                                      IPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAG
SQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKD
                                                                                  MAGLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSG
                                                                                                                                                                  TTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHE
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"Corynebacterium efficiens pyruvate carboxylase (pyc) gene,
CDS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Last annotation update)
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EMBL, AB083299; BAB8803.1;
InterPro; IPR001882; Biotin_attach.
InterPro; IPR005482; Biotin_attach.
InterPro; IPR005492; Biotin_lipoyl.
InterPro; IPR005491; CPase_L_D2.
InterPro; IPR005491; CPase_L_N.
InterPro; IPR005491; CPase_L_N.
InterPro; IPR005491; CPase_L_N.
InterPro; IPR005379; PYC_OADA.
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; biotin_lipoyl; 1.
; CPSase_L_chain; 1.
; CPSase_L_D2; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                  BA7023134519FAAA CRC64;
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                                                                                                           Score 5297.5; DB 2;
Pred. No. 8.1e-275;
44; Mismatches 58;
                                                                  1139 AA; 123068 MW;
PS00188; BIOTIN; 1. PS00867; CPSASE_2; 1.
                                                                                                               90.38;
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Matches 1035; Conservative
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Complete | SEQUENCE
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                          1100 VIVIVAEGDEVKAGDAVAIIEAMKMEATIITASVDGKIERVVVPAATKVEGGDLIVVVS 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCO0546 OR SCF11.26C.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae, Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cerdeno A.W., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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InterPro; IPR000089; Biotin lipoyl.
InterPro; IPR005479; CPase_L_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro IPR005930; Pyruv_carbox. Pfam, PR02785; Blotin_carb_C; 1. Pfam; PP00364; blotin_lipoyl; 1. Pfam; PF00289; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=34(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR005481; CPase_L_N. IPR000891; HMGL-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";
Nature 417:41-147(2002).
EMBL; AL939105; CAB59603.1; -.
HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003379; PYC_OADA.
                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAK-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyruvate carboxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ELVDPLTKLPTASAGEPPAGSRQLLAELGPEGFARRLRESSTIGVTDTTFRDAHQSLLA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 EAASREAASAFGDSTVFLEKAVVEPRHIEVQILADGEGDVIHLFERDCSVQRRHQKVIEL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVTEVDLVKAOMRLAAGATLKELGLTQDKIKTHGAALOCRITTEDPNNGFRPDTGTITAY 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRP 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNI 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVTA 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVIDVDLVQSQLRIAAGQILADLGLAQENIILRGAALQCRITIEDPANGFRPDIGQISAY 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 KDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTFRDAHQSLLA 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLSNLRAQATAL 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLADRFELLEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYDIP 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       928 DSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADDSKERRNSL 987
                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY
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                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                         Length 1124;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                        1FEF4C4643954D31 CRC64;
                                                                                                                                                                                                      Score 3797; DB 16;
Pred. No. 1.5e-194;
                                                                                                                                                                                                                                                         Matches 735; Conservative 156; Mismatches 227;
Pfam; PF02786; CPSase_L_D2; 1.
Pfam; PF00662; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
IIGRPAMS; TIGR01235; Pyruv_carbox; 1.
PROSITE; PS00867; CPSASE_2; 1.
                                                                                                                                                        1124 AA; 121071 MW;
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989 RLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEP 1048
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                AKKAGLPVLAESTPSKNIDDIVKSAEGOTYPIFVKAVAGGGGRGMRFVSSPDELRKLATE 210
                                                 183
                                                                                                                                            271 AQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTEEV 330
                                                                                                                                                                                                            TEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAYRS 390
                                                                                                                                                                                                                                           304 IDVDLVSSQLRIAAGETLADLGLSQDRLVVRGAAMQCRITTEVPANGFRPDTGRITAYRS 363
                                                                                                                                                                                                                                                                         PGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATNIG 450
                                                                                                                                                                                                                                                                                            451 FLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRPKDV 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      629 MILRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAV 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  689 AEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVTAL 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749 RREFDLPVHYHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSAIVAAFAHT 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  869 LADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYDIPD 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADDSKERRNSLN 988
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                                               NRILFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRL-PDVRTPLLVRLDAIS 1046
                                                                             956 NRLLFPGPAREFDTHRASYGDTSILDSKDFFYGLRPGKEYTVDLDPGVR--LLIELQAVG 1013
                                                                                                              1067 EPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFAGVVTVTVAE 1106
                                                                                                                                IDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVTA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Pyruvate carboxylase from Mycobacterium smegmatis: stabilization, rapid purification, molecular and biochemical characterization and regulation of the cellular level.";
Biochim. Biophys. Acta 1475:191-206(2000).
-!- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL, AF262949; AAG30411.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 64.6%; Score 3786.5; DB 2; Length 1127; Local Similarity 66.2%; Pred. No. 5.4e-194; les 747; Conservative 142; Mismatches 233; Indels 7;
                                                                                                                                                                            1107 GDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAATKVEGGDLIV 1154
                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBI_TaxID=1772;
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                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pfam; PF00682; HMGL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
IGRFAMs; TIGR01235; PYUV_Carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS001867; CPSASE_2; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                                                                                                                                                                                                            PRT; 1127
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InterPro; IPR000634; S/T_dehydrtse.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00284; biotin_lipoy1; 1.
Pfam; PF00289; CPSase_L_chain; 1.
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InterPro; IPR005479; Chase_L_D2.
InterPro; IPR005481; Chase_L_D2.
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InterPro; IPR005482; Biotin_carb_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20374587; PubMed-10913817;
Mukhopadhyay B., Purwantinil E.;
                                                                                                                                                                                                                                                                                                                                                                        Pyruvate carboxylase (EC 6.4.1.1).
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Interpro, IPR000891, HMGL-like.
Interpro, IPR003379, PVC_CADA.
Interpro, IPR005930, Pyruv_carbo
                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium smegmatis.
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985 NSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDA 1044
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                                            149 TAAKKAGLPVLAESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLA 208
                                                                                                                                                                                                                                                                                                                                 EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 388
                                                                          182 EAASREAESAFGDPTVYLEQAVINPRHIEVQILADNLGDVIHLYERDCSVQRRHQKVIEL 241
                                                                                                                                                                                                                                                              389 RSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATN 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 IGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRPK 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 LLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPN 624
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                                                                                                                                         209 TEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Hickey E.,
Fleterson J., DeBoy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                         MEDINE-9825987; pubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier I., Churcher C., Harris D.,
Gordon S.V., Egilmeier K., Gas S., Barry C.E., III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Buston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY
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                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains.",
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 283018; CAB05410.1; -.
EMBL; AE007125; AAK47371.1; -.
         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 120.4 kDa protein (Pyruvate carboxylase)
PCA OR RV2967C OR MTCX349.20 OR MT3045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.3%; Score 3713.5; DB 16; 64.4%; Pred. No. 4.3e-190;
                                                                                                                                                                                Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239;
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PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome SEOUENCE 1127 AA; 120422 MW; 84B0A4
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InterPro; IPR00891; WAGL-like.
InterPro; IPR001379; PYC_OADA.
InterPro; IPR005930; PYCU_Carbox.
InterPro; IPR005930; PYCU_Carbox.
Pfam; PF02785; Biotin_carb_C; Pfam; PF02785; Biotin_carb_C; Pfam; PF00364; biotin_lipoyl; I.
Pfam; PF02786; CPSase_L.Chain; I.
Pfam; PF00682; HMGL-like; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001882; Biotin_attach.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR005479; CPase_L_D2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 393:537-544 (1998).
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                         NCBI_TaxID=1773;
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InterPro;
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980 SKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTPLL 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDPPAVPVSAWTAAP----TWRRNQPVLRLHAGQADLSGRDLPTAVSRARRAIAEFRIR 415
                            GVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKPH 503
                                             680 AVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPA 739
                                                                                                                                                                                                                                                                      740 AVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLS 799
                                                                                                                                                                                                                                                                                                                                                                     800 AIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPIGRVYRHEIPGGQLSN 859
                                                                                                                                                                                                                                                                                                                                                                                      860 LRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920 DPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADD 979
                                                                                                                                                                                                                                                                                                                             GVRPKDVAAPIDKLPNIKDLPL----PRGSRDRLKQLGPAAFARDLREQDALAVTDTTFR
                                                                                                                                                         620 EAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAID
                                                                                                                                          DAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pyruvate carboxylase (EC 6.4.1.1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITIEDPNNGFRPDIGTITAY 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1124;
                                                                               Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1124 AA; 120672 MW; 07E1692E12203491 CRC64;
                                                                                                                                                                                                                          Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
-!- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; U00024; AAA50948.1;
                                                                                                                                                                                  Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 59.4%; Score 3484; DB 2; Il Similarity 62.2%; Pred. No. 8.2e-178; 698; Conservative 151; Mismatches 251;
  AA
 PRT; 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIGHERAMS; TIGRO1235; PYTU Carbox; 1.
TIGREAMS; TIGRO1235; PYTUV Carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00867; CFSASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003379; PYC_OADA.
InterPro; IPR0059379; PYC_OADA.
InterPro; IPR005939; Pyruv_carbox.
InterPro; IPR00634; S/T_dehydrtse.
Pfam; PF002785; Biotin_carb_C; 1.
Pfam; PF00289; CPSase_L_Calain; 1.
Pfam; PF02786; CPSase_L_Calain; 1.
Pfam; PF00682; HMGL-like; 1.
                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
                                                                                                                                                                                                                                                                                            Interpro; IPR001882; Biotin_attach.
Interpro; IPR005482; Biotin_carb_C.
Interpro; IPR000089; Biotin_lipoyl.
Interpro; IPR005479; CPase_L_D2.
Interpro; IPR005481; CPase_L.D.
Interpro; IPR000891; HMGL-like.
 PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  P24182;
                                                                                                                                                                     Smith D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329
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             050450;
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and domain structure of chicken pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                          carboxylase.";
Biochem. Biophys. Res. Commun. 295:387-393(2002).
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Query Match
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                                                                                                                                                                                                                                                                                                                                 SEQDIGOMHRQKADEAYLVGRGLPPVQAYLHVPDIIRVARENAVDAIHPGYGFLSERADF 127
                                                                                                                                                                                                                                                                                                                                                                 ARECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVL-AESTPSKNIDDIVKSAEGQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTVEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQL-GGEITAHFDSMLV 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KMICRGSDFETAVARAQRALAEFIVSGVATNIGFLRALLREEDFISKRIATGFIGDHPHL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 FHLRPSQNRAQKLLHYLGHVMVNGPSTPLPVKAKAKAAVVEPVPP----PVPMGSPPBGLRA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664 EVAAANGMDIFRIFDALNYLPNLLLGVEAVGRAG-AVVEAALSYTGDVADFTRTKYSLDY 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 712 YLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLAT 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQACVDAGVRFVGPPPEVVRKMGDKVEARSIAIAAGVPVVPGTSAPVATLGEAQDFAARV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIVEFLVDRDGKHYFIEVNSRLQVEHTVTEEITGVDLVQAQLLVAAGRSLSELGLQQDSV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFV 651
                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQAPPADDEQGRILDYLADVTVNKPHGVRP-KDVAAPIDKLPNIKDLPLPRGS-----RD
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                                                                                                                                                                                                                                                                  7 GGLLLKGIITLV-----STHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIY
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                                                                                                                                                                                                                     DB 13; Length 1178;
                                                                                                                                                                                                                                              33;
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Local Similarity 47.5%; Pred. No. 7.6e-128;
nes 559; Conservative 168; Mismatches 416; Indels
                                                                                                                                                                                            1178 AA; 127253 MW; F0722FEAB8BF39A5 CRC64;
                                                                                                                                                          Pfam; PF02436; PYC_OADA; 1.
TIGRFAMs; TIGR01235; pyruv_carbox; 1.
                               Interpro; IPR005479; CPASe_L_POT: Interpro; IPR005491; CPASe_L_D.
Interpro; IPR005491; MGL-11ke.
Interpro; IPR00591; HMGL-11ke.
Interpro; IPR005379; PYTUV_carbox.
Pfam; PF00364; Biotin_carbox.
Pfam; PF00364; biotin_lipoy1; IPFam; PF00364; Biotin_carbox.
Pfam; PF00364; Biotin_lipoy1; IPFam; PF00692; RMGL-IRE; IPFam; PF00692; HMGL-IKe; I.
          Interpro; IPR005482; Biotin_carb_C.
Interpro; IPR000089; Biotin_lipoyl.
Interpro; IPR005479; CPase_L_D2.
                                                                                                                                                                                            SEQUENCE
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GQIRPMRVRDRSVESVIATAEKADSSNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIE 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1002 HRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVN 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1023 FTSTFGPVSCLGTRLFLEGPTIAEEFEVELERGKT-LHIKALALGDLNAAGQREAFFELN 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    889 RPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEP 948
771 YFAAAQAGADAVDGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVR
                                                                                                                                                                                         GLYLPFESGTPGPTGR--VYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLG
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EMBL; AP001516; BAB06344.1; --
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Last annotation update)
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TIGRFAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00867; CPSASE_2; 1.
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SEQUENCE 1150 A
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Horikoshi K.;
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Q9K9M0
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1027 ILIRLPDVRTPILVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADS 1086
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                                                                                                  86 KAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKS 145
                                                                                                                        325 TVTEEVTEVDLVKAQMRLAAGATL--KELGL-TQDKIKTHGAALQCRITTEDPNNGFRPD 381
                                                                                                                                                                                                                                                                                                                                                                                                                 FRDAHQSILATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDE 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             857
                                                                                                                                                                                                                                                                                265 VVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEH 324
                                                                                                                                                                                                                                                                                                     244 VVEVAPSVSLSEDVRERICQAAVQLAENVNYVNAGTVEFLVDREGNFYFIEVNPRIQVEH 303
                                                                                                                                                                                                                                                                                                                                                           TVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVN 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 KPHGVRPKDVAAPIDK--LPNIK-DLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           678 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR 737
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                                                                          63
                                           26 LPAFKKILVANRGELAVRAFRAALETGAATVALYPREDRGSFHRSFASEAVRIGTEGSPV 85
                                                                        4 LKNIKKVLVANRGEIAIRIFRACTELHIRTVAIYSKEDTGAYHRYKADEAYLVGEGKKPI
                                                                                                                                                                                                                      RKLATEASREABAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQK
                                                                                                                                                                                                                                         146 RAVTAAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 RIRGIKTNIAFLENVVQHRQFLSGEYNTSFIDQTPELFVFPKRKDRGTKMLSFIGETIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 TGTITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     782 ANSLYYALADSEROPNVNITALEOLAEFWEETRKFYAGFESGMNAPHTEVYEHEMPGGOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LREAMPNVNIQMLIRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA
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               27; Gaps
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               Mismatches
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Il Similarity 46.9%; Pre 540; Conservative 185;
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A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Borriss R., Boursier L., Brans A., Braun M., Brigals S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoff A., Erlich S.D., Emmerson P.T.,

RA Denizot F., Carington J., Fabret C., Ferrari E., Foulger D.,

RA Ghims S.Y., Claser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Mieln C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

A Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Resecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Persecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadale Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Takeuchi M., Taccooi E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Taccooi E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Taccooi E., Takagi T., Takahashi H., Takemaru K.,

Rai A., Taccooi E., Pangler E., Wedler F., Vassarotti A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Tosato V., Wambutt R., Wedler E., Wedler H., Weitzeneger T.,

Winters P., Wibat A., Yamamoto H., Yamanoto K., Yasumoto K., Yata K.,

Tah complete genome sequence of the Gram-positive bacterium Bacillus

Rh Fill P. Schikawa H.F., Zunner P., Schikawa H.F., Suhrish E.,

Rh Fill P. Schikawa H.F., Zamamoto H., Kanner F., Ruber F., R
                                                                                                                           1018 IEVEIEQGKT-LIVKFISLSKPQDDGNRIVYFELNGQPREVLIKDQSVKTSIISRPKADK 1076
                                                                         1087 SNKGHVAAPFAG-VYTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAAT 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
EMBL; Z99111; CAB13359.1; -
HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pyruvate carboxylase (EC 6.4.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000089; Biotin_lipoyl InterPro; IPR005479; CPase_L_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98044033; PubMed=9384377;
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InterPro; IPR005930; Pyruv_carbox.
Pfam; PF02785; Biotin_carb_C; 1.
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                                                                                                                                                                                                                                 1146 KVEGGDLIVVV 1156
                                                                                                                                                                                                                                                                                   :: |||:: |
1137 AIQTGDLLIEV 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KWU4;
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Q9KWU4
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---EQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFF 1018
                                                                                                                                                         1019 YGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVT 1078
                                                   914 PADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEE--- 970
            836 GGQYSNLQQQAKGYGLGDRWNEVKEMYRRVNDMFGDIVKVTPSSKVYGDMALYMVQNNLT 895
                                                                                         EKDVYEKGESLDFPDSVVELFKGNIGQPHGGFPEKLQKLILKGQE----PITVRPGELLE 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A. MEDIINE-21100417; PubMed-11167010; Voder J.A., Liftman G.W.; The zebrafish fthl, slcaa2, menl, pc, fgf3 and cycd1 genes define two regions of conserved synteny between linkage group 7 and human chromosome 11q13...;
                                                                                                                                                                                                                                       ||: | | : : : | |: | 1008 YGMTLGEEIEVEIERGKT-LIVKLISIGEPOPDATRVVYFELNGOPREVVIKDESIKSSV
                                                                                                                                                                                                                                                                                              1079 ATAEXADSSNKGHVAAPFAGVVTVTVAE-GDEVKAGDAVAIIEAMKMEATITASVDGKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LGGLLLKGIITLV-----STHTSS-TLP--AFKKILVANRGEIAVRAFRAALETGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 1180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 550; Conservative 179; Mismatches 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.0%; Score 2523.5; DB 1 46.6%; Pred. No. 2.1e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HESP, P24182; 1BNC.
ZFIN; ZDB-GRNE-000831-1; pc.
InterPro; IPR001882; Biotin_carb_C.
InterPro; IPR001882; Biotin_carb_C.
InterPro; IPR005482; Biotin_lipoyl.
InterPro; IPR005493; Biotin_lipoyl.
InterPro; IPR005493; PCase_L_D2.
InterPro; IPR003891; HMGL-like.
InterPro; IPR003891; PCG-ADA.
InterPro; IPR005891; PCG-ADA.
InterPro; IPR005930; PYC_ADA.
InterPro; IPR005930; Pycu_carbox.
Ffam; PF003785; Biotin_carb_C; 1.
Pfam; PF00334; biotin_lipoyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02436; PYC_OADA; 1.
TIGRFAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 261:235-242(2000).
-!- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; AF295372; AAG37836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                       1138 RVVVPAATKVEGGDLIVVV 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00289; CPSase_L_chain; 1. Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyruvate carboxylase
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NCBI_TaxID=7955;
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01-OCT-2002
                                                                                         968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 YLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 VTAAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 LATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 EVAPSVSLSPELRDQICEAAVALAKNVNYINAGTVEFLV-ANNEFYFIEVNPRVQVEHTI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEEVTEVDLVKAQMRLAAGATL--KELGLTQDK-IKTHGAALQCRITTEDPNNGFRPDTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 TEMITGVDIVOTQILVAQGHSLHSKKVNIPEQKDIFTIGYAIQSRVTTEDPQNDFMPDTG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 TITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVN-- 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAV 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDTTFRDAHOSLLATRIRSHDLKKIANPTAALWPELFSMEMWGGATFDVAYRFLKEDPWK 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657 MTLAIDAVRDIG-KVAEAAICYIGDILDKNRTKYDLAYYISMAKELEAAGAHILGIKDMA 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734 GLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTT 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIP 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQPSASGFYHAMEGNDRRPEMNVQGVELLSQYWESVRKYYSEFESGMKSPHTEIYEHEMP 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 854 GGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVD 913
                                                                                                                                                                                                                                                                                                                                   28 AFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 REQAEKAGIPVIPGSDGPAETLEAVEQFCQANGYPIIIKASLGGGGGRGMRIVRSESEVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 AYERAKSEAKAAFGNDEVYVEKLIENPKHIEVQVIGDKQGNVVHLFERDCSYQRRHQKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 PGIGKKEKPAFDKPLGVKVDVDQQP-----ARGTKQILDEKGAEGLANWVKEQKSVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMA
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                 Length 1148;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                      1148 AA; 127936 MW; 98D14DD56F361620 CRC64;
                                                                                                                                                                                                                             cch 43.1%; Score 2530; DB 16; 18 Similarity 46.0%; Pred. No. 9.1e-127; 533; Conservative 188; Mismatches 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGR01235; pyruv_carbox; 1. PROSITE; PS00866; CPSASE_1; 1. PROSITE; PS00867; CPSASE_2; 1.
PF00364; biotin_lipoyl; 1. PF00289; CFSase_L_chain; 1. PF02786; CFSase_L_D2; 1. PF02682; HMGL-like; 1. PF02436; PYC_OADA; 1.
                                                                                                                                                                   Ligase; Complete proteome
                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443
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                                                                                                                                                                                                                               Query Match
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                       Pfam;
Pfam;
                                                                 Pfam;
                                                                                                                                                                                                                                                                       Matches
                                                                                  Pfam:
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16;

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1081 LNGQLRSVLVKDIAAMKEMHFHPKALKDVRGQVGAPMPGKVVEVKVKAGQKVEKGQPLCV 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOTIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.8%; Score 2509; DB 2; llarity 46.8%; Pred. No. 1.2e-125; Conservative 181; Mismatches 397;
                                                                                                                                                                                                                          Firmicutes; Bacillales; Geobacillus.
                                                                                                                            1147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro; IPR001882; Biotin_attach, InterPro; IPR001882; Biotin_attach. InterPro; IPR001899; Biotin_lipoyl. InterPro; IPR005491; CPase_L_D2. InterPro; IPR005481; CPase_L_D2. InterPro; IPR00581; HMGL-like. InterPro; IPR00891; HMGL-like. InterPro; IPR005909; PYC_ADA. InterPro; IPR005909; PYC_ADA. Ffam; PF02785; Blotin_carb_C; IPR05930; Pyruv_carbox. Pfam; PF00354; blotin_lipoyl; I.
                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                             Kondo H., Kazuta Y., Saito A., Fuji
"Cloning and nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGR01235; pyruv_carbox; 1
PROSITE; PS00188; BIOTIN; FALSE_NEG
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                             MEDLINE=97354293; PubMed=9210587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00289; CPSase_L_chain; 1. Pfam; PF02786; CPSase_L_D2; 1. Pfam; PF00682; HMGL-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D83706; BAA12072.1; -. P24182; 1DV1.
                                                                                                                                                     (TrEMBLrel. 03, TrEMBLrel. 03, TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYC_OADA;
                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         pyruvate carboxylase.";
Gene 191:47-50(1997).
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296
1112
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Matches 539; Conserv
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=1422;
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1064
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                                                                                                                                                                                                                                                                                  STRAIN-K1041
                                                                                                                                                     01-MAY-1997
                                                                                                                                                                                                                          Bacteria;
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BINDING
                                                      1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                               RESULT 13
P94448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .000 LEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVAN 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1022 KEFTSTFGPVDCLNTRLFLDGPKIAEEFQVELERGKI-LHIKALALGDLNKSGQREVFFE 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFRSKVLKSLPRIEGR-PGASLPPMDFEALESGLRAAHGDEITPEDVMSAAMYPKVFQEF 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650
                                                                                                                                                                                                                                                                   353
                                                                                                                                                                                                                                                                                                                                                                                                DRLKQLGPAAFARDLREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELL 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
                                                                                            ENAQLARECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVL-AESTPSKNIDDIVK 173
                                                                                                                                                                                                                                                                                                364
                                                                                                                                                                                                                                                                                                                       354 TQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQL-GGEITAHF 412
                                                                                                                                                                                                                                                                                                                                      DSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                    DHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRP-KDVAAPIDK-LPNIKDLPLPRGSR 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            724 YYLKLADELVKAGTHILSIKDMAGLLKPQASRLLIEALRDRFPDIPIHVHTHDTAGAGVA 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        770 TYFAAAQAGADAYDGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAV 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPE 947
                                                                 TVAVYSEQDTGQMHRQKADEAYLIGRGLSPVAAYLHIPDIIKVAKENNVDAIHPGYGFLS 124
                                                                                                                        ERADFAQACAEAGVRFIGPSPEVVRKMGDKVEARALAIKAGVPVVPGTDAPISCLQEAQE 184
                                                                                                                                                                                                         QHIEVQILGDRIGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSI 293
             64
TVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLS
                                                                                                                                                  174 SAEGQIYPIFVKAVAGGGGRGMRFVSSPDELRKLATEASREAERAFGDGSVYVERAVINP
                                                                                                                                                                    GYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 VKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGLYLPFESGTPGPTGR--VYRHEIPGGQLSNLRAQATALGLADRFELTEDNYAAVNEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDLIKVTPSSKIVGDLAQFWV-QNLSRAEVEKRADELSFPLSVVEFLQGHIGIPHGGFPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLRTRALEG--RSEGKAPLTEVPEEEQAHLDA-----DDSKERRNSLNRLLFPKPTEEF
                                                                                                                                                                                                                                    245 RHIEVQILGDKYGNVIHLYERDCSIQRRHQKVVEIAPAAHLDSHLRDRLTLDSVNLAKQV
                                                                                                                                                                                                                                                                                 ENONLFNLKPTQNRAQKLLHYLGHVMVNGPMTPIPVKAKPSPVDPVIPSVSLGEPPLGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVILREGPEGFARAIRQHQGLLLMDTTFRDAHQSLLATRVRTHDLKKIAPYVSHNFSNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLENWGGATFDAAMRFLSECPWKRLQELRALIPNVPFQMLLRGANAVGYTNYPDNAVFKF
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-!- CATALYTIC ACTIVITY: ATP + PYRUVATE + HCO(3)(-) = ADP + ORTHOPHOSPHATE + OXALOACETAIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: BIOTIN (BY SIMILARITY).
-!- PATHWAY: GLUCONEOGENESIS.
-!- SUBCELLULAR GLUCONEOCENESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, PARTICULARLY FROM EUKARYOTES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOTIN CARBOXILASE (BY SIMILARITY).
CARBOXYLTRANSFERASE (BY SIMILARITY).
BIOTIN CARBOXIL CARRIER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.-I.;
Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                           vi-Mak-2003 (TrEMBLrel. 23, Last annotation update)
Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1147;
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                                          1119 IEAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVVS 1157
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IQAGDLIMELS 1146
                                                                               1147 VEGGDLIVVVS 1157
                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5061;
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1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1028 LIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSS 1087
                                                                                                                         618
                                                                                               DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149
                                                                                                                                                                                                                                                                                                                                                      APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLV--DEKGNHVFIEMNPRIQVEHTV 326
                                                                                                                                                                                                                                                                                                                                                                                          247 APSVSLSDELRQRICEAAVQLMRSVGYVNAGTVEFLVSGDE---FYFIEVNPRIQVEHTI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 IITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVAINIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503 HGVRPKDVAAPI---DKLPNIKDL-PLPRGSRDRLKQLGPAAFARDLREQDALAVTDITF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAAHVLISGLKETVDIPIYLHTHDISGNGIYTYAKAIEAGVDIVDVAISSMAGLISQPSA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   919 ADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDAD 978
                                                                                                                                                                              150 AAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRKLA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                      327 TEEVTEVDLVKAQMRLAAGATL--KELGL-TQDKIKTHGAALQCRITTEDPNNGFRPDTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRP 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                739 AAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSL 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLS 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERGETLNPPDSVVELFEGYLGQPHGGFPKELQRIILKGRE----PITVRPGELLEPVDFE 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFA 918
                                       KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL
                                                                                                                                                                                                                                                                  209 TEASREABAAFGDGSVYVERAVINPQHIEVQILGDRTGEVVHLYERDCSLQRRHQKVVEI
                                                                                                                                                                                                                                                                                          RDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDEL
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NKGHVAAPFAG-VVTVTVAREGDEVKAGDAVAIIEAMKMEATITASVDGKIERVVVPAATK 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTPEVLDLTGDKSRAVTAAKKAGLPVLAEST-PSKNIDDIVKSAEGQTYPIFVKAVAGGG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 YERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNH 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 STHT----SSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus niger,
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MAIN.

A Panneman H., Ruijter G.J.G., Van den Broeck H.C., Visser J.;

Raspergillus niger pyruvate carboxylase.";

Submitted (JUL-1988) to the EMBL/GenBank/Doby databases.

-!- COFACTOR: BIOTIN (BY SIMILARITY).

EMBL, AJ00972; CAC19838.1;

R HSSP, P24182; IBNC

InterPro; IPR001882; Biotin_attach.

R InterPro; IPR001882; Biotin_acarb_C.

R InterPro; IPR005479; CPase_L_D.

R InterPro; IPR005479; CPase_L_N.

R InterPro; IPR00549; CPase_L_N.

R InterPro; IPR00549; PYTUV_CAAD.

R InterPro; IPR005419; PYTUV_CAATOX.

R InterPro; IPR005910; PYTUV_CAATOX.

R Pfam; PF00786; Biotin_lipoyl; 1.

R Pfam; PF00786; Biotin_lipoyl; 1.

R Pfam; PF00789; CPasse_L_Chain; 1.

R Pfam; PF00789; CPasse_L_Chain; 1.

R Pfam; PF00789; CPasse_L_Chain; 1.

R Pfam; FP00789; PYTUV_CAATOX.

R Pfam; PF00789; CPasse_L_Chain; 1.

R Pfam; PF00789; PYTUV_CAATOX.

R Pfam; PF00789; CPasse_L_Chain; 1.

R Pfam; PF00789; CPasse_L_Chain; 1.

R Pfam; PF00789; PYTUV_CAATOX.

R Pfam; PF00789; PYTUV_CAATOX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Pyruvate carboxylase (EC 6.4.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1192 AA.
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Bacillales; Listeriaceae; Listeria

NCBI_TaxID=1639;

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STRAINEEGD-6 / Serovar 1/2a;

XX MEDLINE=2153729; PubMed=11679669;

RA MEDLINE=21537279; PubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Clay E., de Daruvar A., Deboux P.,

Charbit A., Chetcuani F., Couve E., de Daruvar A., Deboux P.,

Domann B., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fishi H., Garcia del Portillo F., Garrido P.,

Rautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

An Jones L. H., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

An Madueno E., Maitournam A., Mata Vicente J., Noy E., Nedjari H.,

Nordslek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simces N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";

EMBL, AL591977; CAC99150.1; -.

RICEPPO: IPR00089; Biotin lipoyl.

RICEPPO: IPR00189; HMGL-lipoyl.

RICEPPO: IPR00189; PVC_OADA.

RICEPPO: IPR00189; PVC_OADA.

RICEPPO: IPR00189; PVC_OADA.

RICEPPO: IPR00189; PVC_OADA.

Pfam: PF00286; Biotin_carb C.

Refam: PF00386; Biotin_carb C.

Refam: PF00786; CPSase_LDCAIN;

Refam: PF00786; PR00789; PVC_DAIN;

Refam: PF00786; PVC_DAIN;

Refam: PVC_DAIN T.

Refam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02436; PYC_OADA; 1.
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Pfam; PF00682; HMGL-like;
        Listeria monocytogenes.
                         Bacteria; Firmicutes;
                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                            490
EDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQLGGE-ITAHFDSMLVKMTCRGSDFETAV 430
                                                                                                                                                                                                                                                                                                                                                                                                                               626
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                                                                                                                                                                                                                                               RKVVRALVEFRIRGVKTNIPFLISLLSHPVFVDGTCWTTFIDDTPELFALVGSQNRAQKL
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                                                           VFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITT
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90 DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 APCNAITSELRNRICDAAVKLMKNVDYINAGTVEFLV-EGDDFYFIEVNPRVQVEHTITE 303
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                                                                                                                                                                                                                                                                                                                1146 AA; 128049 MW; A062F88C9A092B6F CRC64;
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IIGRFAMS; IIGR01235; pyruv_carbox;
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
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Last sequence update)
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01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,

Q8Y846 ID Q6 AC Q6 DT 01 DT 01 DE P3

PycA protein. PYCA OR LMO1072.

PRELIMINARY;

Q8Y846 Q8Y846;

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981 K------ERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLI 1029
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                                                                                                         561 AHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELRE 620
                                                                                                                                                                   680
                                                                                                                                                                                                                    681 VLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAA 740
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                                                                                                                                                                                                                                                                                             801 IVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLSNL 860
                                                                                                                                                                                                                                                                                                                                                 861 RAQATALGLADRFELIEDNYAAVNEMLGRPTKYTPSSKVVGDLALHLVGAGVDPADFAAD 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 GDTIDFPDSVIEFFMGEIGQPYGGFPEKLQKLVLKGRT----PLTDRPGALMEPVNFVDV 956
                                                                                                                         602 QIPNVMFQMLLRGANAVGYKNYPDNVIREFVKQSAQSGVDVFRVFDSLNWIKGMEVSIDA 661
445 VATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLADVTVNKPHG 504
                                                                        621 AMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDA
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1136 SGDLLIEVN 1144
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Search completed: September 24, 2003, 15:59:11 Job time: 95.6587 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 24, 2003, 15:51:28; Search time 88.3413 Seconds (without alignments) 3330.038 Million cell updates/sec Run on:

US-09-974-973A-19 ritle:

1 MSTHTSSTLPAFKKILVANR.....RVVVPAATKVEGGDLIVVVS 1140 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

sp_archea:* sp_bacteria:* SPTREMBL_23:*

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_vertebrate:* sp_bacteriap:* sp_organelle:* sp_archeap:* sp_plant:*
sp_rodent:* sp_rvirus:* sp_mammal:* sp_mhc:* sp_virus:* sp_phage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	054587 corynebacte	081294 corynebacte	08frq0 corynebacte	O8rgl2 corynebacte	09rk64 streptomyce	O9f843 mycobacteri	P95127 mycobacteri	Q50450 mycobacteri	08jhf6 qallus qall	Q9k9m0 bacillus ha	Q9kwu4 bacillus su	Q9ddt1 brachydanio	Q9hes8 asperdillus	P94448 bacillus st	Q8y846 listeria mo	Q97fr7 clostridium
		1	054587	Q8L2G4	Q8FRQ0	QBRQL2	09RK64	Q9F843	P95127	050450	Q8JHF6	Q9K9M0	Q9KWU4	Q9DDT1	Q9HES8	P94448	Q8Y846	Q97FR7
		BB	16	~	16	~	16	7	16	7	13	16	16	13	m	7	16	16
		Match Length DB	1140	1140	1168	1139	1124	1127	1127	1124	1178	1150	1148	1180	1192	1147	1146	1144
æ	Query	Match	100.0	99.5	91.9	91.7	65.6	65.4	64.1	60.2	44.1	43.6	43.6	43.5	43.4	43.3	43.1	43.0
		Score	5788	5759	5317.5	5305.5	3799	3783.5	3712.5	3483	2552	2525.5	2524	2519.5	2509.5	2505	2493	2491.5
	Result	No.	-	7	3	4	ហ	9	7	6 0	ወ	10	11	12	13	14	15	16

17 2490 43.0 1146 16 092CWI 19 2489 43.0 1150 16 0RNX69 19 22488 43.0 1150 16 0RNX69 20 2487.5 42.0 1150 16 0RX710 22 2477.5 42.8 1158 16 0RFYIO 22 2477.5 42.7 1174 16 0RFYIO 22 2470.5 42.7 1152 16 0RFYIO 24 2464 42.6 1153 16 0RCPM3 24 241 42.2 1175 5 01773 2 2437.5 42.1 1175 5 01773 3 0RY720 30 2437.5 42.1 1175 3 0RY713 31 2435 42.1 1185 3 0RYII3 32 2435 42.1 1185 3 0RRWF 2419 41.8 1195 5 0RRWF 240 41.5 1137 16 0RRWF 240 41.5 1100 19.0 525 5 0RRWF 240 1100 19.0 521 5 0RRWF 24	Q99cw1 listeria in Q8nx69 staphylococ Q99318 aspergillus Coc Q99318 aspergillus Su Q8fftO brucella su Q8fftO brucella me Q8f20 brucella me Q8f20 brucella me Q8732 caenorhabdi Q8ayn3 pagrus majo Q9x20 drosophila Q9x113 pichia angu Q9x113 pichia angu Q92113 rhizobium m P7882 schizosacch Q9xx0 drosophila Q16921 achizobium m P7882 schizobium m Q86x13 pichia angu Q92113 rhizobium m Q86x13 pichia angu Q9x113 pichizobium e Q8x45 drosophila Q16921 achizobium e Q8x46 pagrus majo Q9x41 bacillus su Q8by40 brizobiuus e Q6x043 mus musculu Q8kwu5 bacillus su Q8by44 drosophila
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	11110000000000000000000000000000000000

ALIGNMENTS

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STRAIN-ATCC 13032;
Peters-Wendisch P.G., Kreutzer C., Kalinowski J., Patek M., Sahm H.,
                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                                                      Stephanopoulos G.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              Eikmanns B.J.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                           STRAIN=21253;
Koffas M.A.G., Ramamoorthi R., Pine W.A., Sinskey A.J.,
                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                Corynebacterium glutamicum (Brevibacterium flavum).
                         PRT; 1140 AA.
                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P24182; 1BNC.
INCEPTO: IPR001089; Biotin_attach.
InterPro: IPR001089; Biotin_attach.
InterPro: IPR001089; Biotin_carb_C.
InterPro: IPR000089; Biotin_lipoyl.
                                                                                    Pyruvate carboxylase (EC 6.4.1.1). PYC OR CGL0689.
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=1718;
                         054587
RESULT 1
              054587
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SEQUENCE FROM N.A.
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123102 MW; 2A6D4B4ED2FEB531 CRC64;
                                                                                                                                                              DB 16;
                                                                                                                                                           100.0%; Score 5788; DB 16;
100.0%; Pred. No. 1.9e-302;
ive 0; Mismatches 0;
                                                                                                   TIGRRAMS; TIGR01235; pyruv_carbox; 1. PROSITE; PS00188; BIOTIN; 1. PROSITE; PS00867; CPSASE_2; 1.
                                    InterPro: IPR005930; Pyruv_carbox. Pfam; PP00785; Biotin_carb_C; 1. Pfam; PP00364; biotin_lipoyl; 1. Pfam; PP00289; CPSase_L_chain; 1. Pfam; PP00786; CPSase_L_D2; 1. Pfam; PP00436; PYC_OADA; 1.
                                                                                                                                Biotin; Ligase; Pyruvate; Complete
SEQUENCE 1140 AA; 123102 MW; 2A
                            InterPro; IPR003379; PYC_OADA.
                                                                                                                                                                     Best Local Similarity 100.
Matches 1140; Conservative
IPR005479; C
IPR005481; C
IPR000891; I
                   InterPro;
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DDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1020
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LSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840
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                          SNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF
                                                                                                                            SNERAOATALGLADREELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF
                                                                                                                                                                                                   AADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium crenatum.
Bacteria, Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=168810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang J., Ding J., Liu Y.;

"Cloning and Expression of Pyruvate Carboxylase Gene in Cloning and Expression of Pyruvate Carboxylase Gene in Corynebacterium creatum CD945.";

Submitted (April 2002) to the EMBL/GenBank/DDBJ databases.

EMBL: AF503915; AAM27458.1; --

InterPro: IPR001892; Biotin_attach.

InterPro: IPR004842; Biotin_lipoyl.

InterPro: IPR005482; Biotin_lipoyl.

InterPro: IPR005492; GPase_L_D2.

InterPro: IPR005479; CPase_L_D2.

InterPro: IPR005479; CPase_L_N.

InterPro: IPR00379; PXC_OADA.
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PROSTIE; PS00188; BIOTIN; 1.
PROSTIE; PS00467; CPSASE 2: 1.
SEQUENCE 1140 AA; 123126 MW; FFA90BB7644C910E CRC64;
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Pred. No. 6.9e-301;
5; Mismatches 3;
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PF02786; CPSase_L_D2; 1.
PF00682; HMGL-like; 1.
PF02436; PYC_OADA; 1.
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Best Local Similarity 99.3
Matches 1132; Conservative
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Db Oy Db

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IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV
                                                                                                                IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR
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              LORRHOKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN
                                                                                                                                                                                                      PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG
                                                                                                                                                                                                                     FRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRAL
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                                                               VASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCS
                                                                                                                                                                                                                                                                                                           AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADV
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                                                 LDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRF
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qa Xa

Qγ

g

Oy Oy 셤

DP QY DP δ

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LTGDKSRAVTAAKKAGLPVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRHQKVVEIAPAQHLDPELRDRICADAVKFCKSIGYQGAGTVEFLVDEAGNHVFIEMNPR
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                                                                                                                                                                                                                                                                                 Corynebacterium efficiens YS-314.";
                                                                                                                                                                                                                                          Nakamura Y.,
A., Nishio Y.,
                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 1168;
                                                                                                                                                                                                                                     Nakamura Y
                                                                                                                                           Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                          56; Indels
                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-TS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN-TS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN-TS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN-TS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Ikao K., Sucuti M., Mashima J., Itoh T., Yamagishi A., N Usuda Y., Sugimoto S.;
"The entire genomic sequence of Corynebacterium efficien Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AP003216; BAC17719.1; -..
Ligase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                             1168 AA; 126245 MW; A5D5A4DD4DF285F8 CRC64;
                                                                                                                                                        Corynebacterineae; Corynebacteriaceae; Corynebacterium
NCBI_TaxID=152794;
                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        91.9%; Score 5317.5; DB 10
91.2%; Pred. No. 3.8e-277;
iive 43; Mismatches 56;
              1168
                                               Created)
                                                                                          Pyruvate carboxylase (EC 6.4.1.1)
PYC OR CE0709.
                                            01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                         Corynebacterium efficiens.
                                                                                                                                           Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                PRELIMINARY;
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Matches 1038; Conserv
                               Q8FRQ0;
01-MAR-2003
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VRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFAGV 1082
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                                                                                                                                                                                                                                                                                                                                                                                               AATKLVTALRREFDLPVHVHTHDTAGGQLATYLAAANAGADAVDAASAPLSGTTSQPSMS
                                                                                                                                                                             AVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPA
                                                     AVTKLVIALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLS
                                                                                                          AIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLSN
                                                                                                                                                              LRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAA
                                                                                                                                                                                                                DPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADD
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"Corynebacterium efficiens pyruvate carboxylase (pyc) gene, complete
"For" "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-1- COFACTOR: BLOTIN (BY SIMILARITY).
EMBL; AB083299; BAB88903.1; -.
INTEPPO: IPRO01882; Biotin_attach.
InterPro; IPR005482; Biotin_carb_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1139 AA
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TIGREAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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InterPro; IPR00549; Crase_L_D2.
InterPro; IPR005481; Crase_L_D.
InterPro; IPR00891; HMGL-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003379; PYC_OADA.
InterPro; IPR005930; Pyruv_carbox.
Pfam; PF002785; Biotin_carb_C; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00289; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123068 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium efficiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyruvate carboxylase.
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01-MAR-2003
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DDSKERRNSLNRLLFPKPTEEFLEHRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AADPOKYDIPDSVIAFLRGELGTPPGGWPEPLRTRALEGRSOGKAPLAEIPAEEQAHLDS
                                               MSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVR
                                                                    MVTTTPSTLPAFKKILVANRGEIAVRAFRAAYETGAATVAIYPREDRGSFHRSFASEAVR
                                                                                                                                      LDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRF
                                                                                                                                                                                 VASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCS
                                                                                                                                                                                                                                                                                                                      FRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL
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                         Gaps
                         1;
 Length 1139;
                         Indels
  DB 2;
                         59;
Score 5305.5; DB 2
Pred. No. 1.6e-276;
                         43; Mismatches
  91.7%;
91.0%;
                      Matches 1037; Conservative
  Query Match
Best Local Similarity
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                                                                                                                                  12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY
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                      proteome.
1124 AA; 121071 MW; 1FEF4C4643954D31 CRC64;
                                                                65.6%; Score 3799; DB 16;
llarity 65.2%; Pred. No. 1.4e-195;
Conservative 154; Mismatches 228;
     PS00867; CPSASE_2; 1.
                                                                                  Similarity
                                                                                                736;
                                   SEQUENCE
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LLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wletzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hopwood D.A.;
"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939105; CAB59603.1; -...
HSSP; P24182; 1BNC.
InterPro; IPRO65482; Biotin_carb_C.
                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                           Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1902;
                                                                                                                                                                                PRT; 1124 AA.
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IIGRFAMs; TIGR01235; pyruv_carbox; 1.
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InterPro; IPR005930; Pyruv_carbox.
Pfam; PF02785; Biotin_carb_c; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_chain; 1.
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InterPro; IPR005479; CPase_L_D2.
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InterPro; IPR000891; HMGL-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00682; HMGL-like;
                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                          Pyruvate carboxylase.
SC00546 OR SCF11.26C.
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MEDLINE-20374587; PubMed=10913817;
MEDLINE-20374587; PubMed=10913817;
Mukhopadhyay B., Purwantinil E.;
"Pyruvate carboxylase from Mycobacterium smegmatis: stabilization,
"Pyruvate carboxylase from Mycobacterium smegmatis: stabilization,
rapid purification, molecular and biochemical characterization and
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                                                                                                                                                                                                                                                 1074 GDEVEAGATVATIEAMKMEASITAPKSGTVTRLAINRIQQVEGGDLLV 1121
                                                                                                                                                                                                             1090 GDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIV 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium smegmatis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Biochim. Biophys. Acta 1475:191-206(2000).
!- COFACTOR: BIOTIN (BY SIMILARITY).
BENBL, AF262949; AAG30411.1;
HSSP; P24182; 1BNC.
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InterPro; IPR001882; Biotin_carb_C.
InterPro; IPR000482; Biotin_carb_C.
InterPro; IPR005481; Biotin_carb_C.
InterPro; IPR005491; CPase_L_D2.
InterPro; IPR005481; CPase_L_D3.
InterPro; IPR005911; HMGL-like.
InterPro; IPR005930; PYCUADA.
InterPro; IPR005930; INTERPRO; INT
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TIGRRAMS; TIGR01235; Pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00867; CPSASE_2; 1.
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Biotin; Ligase
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ASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVEIAP 253
                                                                                  AQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTEEV 313
                                                                                                                                                                    314 TEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAYRS 373
                                                                                                                                                                                                 PGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATNIG 433
                                                                                                                                                                                                                                                                                    FLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRPKDV 493
                                                                                                                                                                                                                                                                                                                                                                        494 AAPIDKLPNIKDL--PLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTFRDAHQSLLAT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIQ 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAV 671
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                                                                                                           184 ASREABSAFGDASVYLEQAVLNPRHIEVQILADGAGNVMHLFERDCSVQRRHQKVVELAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVTAL
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(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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|SEPDERGMRIYMCILNGQLRPVLVRDRSIASAVPAAEKADRGNPGHIAAPFAGVVIVGV 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSINRLLFPKFTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLFDVRTFLLVRLDA 1027
                                                             EAASREAESAFGDPTVYLEQAVINPRHIEVQILADNLGDVIHLYERDCSVQRRHQKVIEL 241
                                                                                                                                                                                                                                                     TEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVEI 251
                                                                                                    APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 311
                                                                                                                       EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 371
                                                                                                                                                                                        RSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATN 431
                                                                                                                                                                                                                                                                                                  IGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRPK 491
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      122 AAAREAGLPVLMSSAPSASVDELLSVAAGMPFPLFVKAVAGGGGRGMRRVGDIAALPEAI 181
                                                                                                                                                                                                                                                                                                                                  IPFLQAVLDDPDFRAGRVTTSFIDERPQLLTARASADRGTKILNFLADVTVNNPYGSRPS 481
                                                                                                                                                                                                                                                                                                                                                                                                                                  LLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPN 607
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                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Gwinn M.L., Haff D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ernolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSKVLVANRGEIAIRAFRAAYELGVGTVAVYPYEDRNSQHRLKADESYQIGDIGHPVHAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                           MEDLINE=9829587; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd & Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeper K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 1127;
                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.",
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Z83018; CABO5410.1;
EMBL; AE007125; AAK47371.1;
HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84B0A4CC1A23CD90 CRC64;
Hypothetical 120.4 kDa protein (Pyruvate carboxylase)
PCA OR RV2967C OR MTCY349.20 OR MT3045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.1%; Score 3712.5; DB 1-64.4%; Pred. No. 6.3e-191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 64.4%; pred. No. 6.3e-
Matches 730; Conservative 153; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein, Complete proteome. SEQUENCE 1127 AA; 120422 MW; 84B0A40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; Profest; HMGL-like; 1.
Pfam; PF00682; HMGL-like; 1.
TIGRFAMs; TIGR01235; PYC_OADs; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00867; CPSASE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculist; Rv2967c; -
InterPro; IPR001882; Biotin_attach.
InterPro; IPR005482; Biotin_carb_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR005479, CPsse_L_D2.
InterPro; IPR005481; CPsse_L_N.
InterPro; IPR000891; HMGL-1ke.
InterPro; IPR003379; PYC_OADA.
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InterPro; IPR000634; S/T_dehydrtse.
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PF00364; biotin_lipoyl; 1.
PF00289; CPSase_L_chain; 1.
                                     Mycobacterium tuberculosis.
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishai W.;
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Pyruvate carboxylase (EC 6.4.1.1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 GVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVNKPH 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 TAAKKAGLPVLAESTPSKNIDEIVKSAEGQIYPIFVKAVAGGGGRGMRFVASPDELRKLA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 TEASREABAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVEI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 RSPGGAGVRLDGAAQLGGEITAHFDSMLVKM-----TCRGSDFETAVARAQRALAEFTVS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FSKVLVANRGEIAIRAFRAAYELGVGTVAVYPYEDRNSQHRLKADESYQIGDIGHPVHAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1124;
                                 Bācteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       07E1692E12203491 CRC64;
                                                                                                                                                   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; U00024; AAA50948.1; -.
                                                                                                        to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.2%; Score 3403; 22.3; Best Local Similarity 62.2%; Pred. No. 1.3e-178; Matches 698; Conservative 151; Mismatches 251;
                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00867; CPSASE_2; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGR01235; pyruv_carbox; 1. PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                InterPro; IPR005930; Pyruv_carbox. InterPro; IPR00634; S/T_dehydrtse. Pfam; PF02785; Bictin_carb_C; I Pfam; PF00364; bictin_lipoy1; 1.
                                                                                                                                                                                              Interpro; IPR001882; Biotin_attach.
Interpro; IPR005482; Biotin_carb_C.
Interpro; IPR006089; Biotin_lipoyl.
Interpro; IPR006479; CPase_L_D2.
                                                                                                                                                                                                                                                                                                                               PF00289; CPSase_L_chain; 1.
PF02786; CPSase_L_D2; 1.
PF00682; HMGL-11ke; 1.
PF02436; PYC_OADA; 1.
                                                                                                                                                                                                                       InterPro; Lravever.
InterPro; IPR005479; CPase_L_uz.
InterPro; IPR005481; CPase_L_N.
TOPA00891; HMGL-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1124 AA; 120672 MW;
                                                                                                                                                                                                                                                                      PYC_OADA.
                       Mycobacterium tuberculosis.
                                                                                                      Submitted (JAN-1994)
                                                                                                                                                                                                                                                         InterPro; IPR000891;
InterPro; IPR003379;
InterPro; IPR005930;
                                                                              SEQUENCE FROM N.A.
                                                                                                                             SEQUENCE FROM N.A.
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                                                          NCBI_TaxID=1773;
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1023 VRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFAGV 1082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 GVSTNIPFLQAVLDDPDFRAGRVTTSFIDERPQLLTARASADRGTKILNFLADVTVNNPY 475
                                                   GVRPKDVAAPIDKLPNIKDLPL----PRGSRDRLKQLGPAAFARDLREQDALAVTDTTFR 542
                                                                                                                                                         543 DAHQSLLATRYRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELR 602
                                                                                                                                                                                   EAMPNVNIQMLLRGRNTVGYTFYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAID 662
                                                                                                                                                                                                                                                                                            592 AAMFNICLQMLLRGRNTVGYTPYPEIVTSAFVQEATATGIDIFRIFDALNNIESMRPAID 651
                                                                                                                                                                                                                                                                                                                                                                              AVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPA 722
                                                                                                                                                                                                                                                                                                                                                                                                             723 AVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLS 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    783 AIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLSN 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             843 LRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAA 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADD 962
                                                                                  476 GSRPSTI-YPDDKLP---DLDLRAAPPAGSKQRLVKLGPEGFARWLRESAAVGVIDITFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and domain structure of chicken pyruvate
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SEQUENCE FROM N.A.
MEDLINE=22145742; PubMed=12150961;
Jitrapakdee S., Nezic M.G., Cassady A.I., Khew-Goodall Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1083 VIVIVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVV 1124
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01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL, AF509529; AAM92771.1; -.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR00069; Biotin_lipoyl.
InterPro; IPR005479; CPase_L_D2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 LQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 RKMGDKVEARSIAIAAGVPVVPGTSAPVATLGEAQDFAARVGFPIIFKAAHGGGGRGMRA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAEFTVSGVAINIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLAD 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 WAVNGPSTPLPVKAKAAVVEPVPP----PVPMGSPPEGLRAVLQREGPAGFARALRGHRG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRPDIGIITAYRSPGGAGVRLDGAAQL-GGEITAHFDSMLVKMICRGSDFETAVARAQRA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 FQPDTGRIEVFRSGEGMGIRLDGASAFQGALISPHYDSLLVKVIAHGPDQPSAAAKMSRA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTVNKPHGVRP-KDVAAPIDKLPNIKDLPLPRGS-----RDRLKQLGPAAFARDLREQDA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534 LAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFED 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       563 LLLXDITFRDAHQSLLATRVRTRDLARIAPFVAHSLSPLCSMETWGGATFDVAMRFLHEC 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     594 PWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALND 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 VSOMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIK 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   714 DMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPL 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 742 DMAGLLTPAAARLLVSSLRDRFPDVPIHVHTHDTAGAAIATLLAAANADADVVDVAVDAM 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  773 SGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGR--V 830
                                                                                                                                                                                                                                                                                                          2 STHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VASPDELRKLATEASREAERAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                           Length 1178;
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                                                                                                                                                                                           1178 AA; 127253 MW; F0722FEAB8BF39A5 CRC64;
                                                                                                                                                                                                                        44.1%; Score 2552; DB 13;
llarity 48.1%; Pred. No. 1.5e-128;
Conservative 165; Mismatches 410;
                                                                                                                                                             TIGREAMS; TIGR01235; pyruv_carbox; 1.
                                           InterPro; IPR005930; Pyruv_carbox. Pfam; PF02785; Biotin_carb_C; 1. Pfam; PF00364; biotin_lipoyl; 1. Pfam; PF00289; CPSase_L_chain; 1. Pfam; PF02786; CPSase_L_b2; 1. Pfam; PF00682; HMGL-like; 1.
IPR005481; CPase_L_N. IPR000891; HMGL-like. IPR003379; PYC_OADA.
                                                                                                                                              PYC_OADA;
                                                                                                                                                                                                                                        Local Similarity
les 556; Conserv
                                                                                                                                            PF02436;
                                 InterPro;
                InterPro;
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1042 PTIABEFEVELERGKT-LHIKALALGDLNAAGQREAFFELNGQLRSILVRDTQALKEMHV 1100
                                                                                                                                  949 EVPEERQA---HLDADDS--KERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYG 1003
                                                                                                                                                                                                       1004 LVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTAT 1063
                                                                                                                                                                                                                                                                                           1101 HPKADRSAKGQVGAPMPGEVVEVRVKEGEAVEKGAPLCVLSAMKMETVYTAPRGGTVSRL 1160
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                 YRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHL 8900
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                                                                                      982 LPPLDFEALSQELGARDGTPPSPEDLLSAALYPKVYAEFRDFTSTFGPVSCLGTRLFLEG
                                                                                                                                                                                                                                                                       1064 AEKADSSNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRV
                                                                  891 VGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEG--RSEGKAPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
Takami H., Makasone K., Takaki Y., Maeno G., Sasaki R., Masui Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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43.6%; Score 2525.5;
Best Local Similarity 46.8%; Pred. No. 3.9e-
Matches 539; Conservative 185; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR0005482; Biotin_carb_C.
Interpro; IPR00089; Biotin_lipoyl.
Interpro; IPR000841; CPase_L_D2.
Interpro; IPR000841; CPase_L_D2.
Interpro; IPR000891; BMGL-like.
Interpro; IPR000891; PVC_OADA.
Interpro; IPR005391; PVC_OADA.
Interpro; IPR005391; PVC_OADA.
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Pfam; PF02786; CPSase_L_D2; 1.
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TIGR01235; pyruv_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyruvate carboxylase.
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RA MIDSTER, Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA ALUBELE-SOVARUS); Fulmed-28743/;
RA ALGERIA S. DOUZIEL L. BEAGN A., Braun M., Brighell S.C., Bron S.,
RA BOTISS R., Boursier L., Brans A., Braun M., Brighell S.C., Bron S.,
RA BOTISS R., Boursier L., Connerton I.F., Capuano V., Carter N.M.,
RA BOTISS R., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dustenhoft A., Ehrlich S.D., Emmerson P.T.,
RA FILEZ C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan B., Puji C., Pornelle D., Roch M., Sadaie Y.,
RA Sarco V., Pohl T.M., Portetelle D., Roch M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Mambutt R., Wedler E., Rahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Tarakanshi H., Takemaru K.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yasaarotti A.,
Wambutt R., Wambutten B., Stone K., Yasamoto K., Yata K.,
Wambutt R., Yoshikawa H.F., Zumatein Bacillus
RA Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Wihters P., Wipat A., Yamamoto H., Weitzenegger T.,
Wihters P., Wipat A., Yamamoto H., Weitzenegger T.,
Whiters P., Wipat A., Yamamoto G. the Gram-Positive B., Positive M.,
 1077 SNPNHIGASMPGIVVKALVEKGDKVKQGDHLMITEAMKMETTVQAPFDGEVVALHVKDGD 1136
                                                                                                                                                                                                                                                                                            Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 29111; CAB13359.1; -.
HSSP; P24182; IBNC.
                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pyruvate carboxylase (EC 6.4.1.1).
                                                                                                                                                                   1148 AA.
                                                                                                                                                                     PRT;
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InterPro, IPR000089; Biotin_lipoyl.
InterPro, IPR005479; CPase_L_D2.
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MEDLINE=98044033; PubMed=9384377;
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InterPro; IPR003379; PYC_OADA.
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                                        1129 KVEGGDLIVVV 1139
                                                                        1137 AIQTGDLLIEV 1147
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                                                                                                                                                                   PRELIMINARY;
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KAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLIGDKS
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                                                                                                                                                                                                                                                            71 YLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRA 130
                                                                                                                                                                                                       131 VTAAKKAGLPVLAEST-PSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRK 189
                                                                                                                                                                                                                      125 REQAEKAGIPVIPGSDGPAETLEAVEQFGQANGYPIIIKASLGGGGRGMRIVRSESEVKE 184
                                                                                                                                                                                                                                                                                           EIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTV 309
                                                                                                                                                                                                                                                                                                                                     310 TEEVTEVDLVKAQMRLAAGATL--KELGLTQDK-IKTHGAALQCRITTEDPNNGFRPDTG 366
                                                                                                                                                                                                                                                                                                                                                   367 IITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAV 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWD 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537 IDTTFRDAHQSLLATRIRSHDLKKIANPTAALWPELFSMEMWGGATFDVAYRFLKEDPWK 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRPAIDAVLEINTAVAEVAMAYSGDLSDPNEKLYILDYYLKMAEEIVKSGAHILAIKDMA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTT 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGQLSNIRAQATALGLADRFELIEDNYAAVNEMIGRPTKVTPSSKVVGDLALHLVGAGVD 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             897 PADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEE--- 953
                                                                                                                   11 AFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKA 70
                                                                                                                               484 PGIGKKEKPAFDKPLGVKVDVDQQP-----ARGTKQILDEKGAEGLANWVKEQKSVLL
                                                                                                                                                                                                                                                                                                                                                                                             SGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVN--
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                                                                        ch 43.6%; Score 2524; DB 16; ll Similarity 46.0%; Pred. No. 4.7e-127; 533; Conservative 186; Mismatches 392;
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                                                     1148 AA; 127936 MW;
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 Pfam; PF02436; PYC_OADA; 1.
                                        Ligase; Complete proteome
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------EQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFF 1001
896 EKDVYEKGESLDFPDSVVELFKGNIGQPHGGFPEKLQKLILKGQE----PITVRPGELLE 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 VRIGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoder J.A., Lithman G.W.;

"The zebrafish fth1, slc3a2, men1, pc, fgf3 and cycd1 genes define two regions of conserved synteny between linkage group 7 and human chromosome 11q13.";
Gene 261:235-242(2000).
                                                                                         952 PVSFEAIKQEFKEQHNLEISD----QDAVAXALYPKVFTDYVKTTESYGDISVLDTPTFF
                                                                                                                                                               1002 YGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGGIRPMRVRDRSVESVT
                                                                                                                                                                                                                                                                          1062 ATABKADSSNKGHVAAPFAGVVTVTVAE-GDEVKAGDAVAIIEAMKMEATITASVDGKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 STHTSS-TLP--AFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 1180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.5%; Score 2519.5; DB 1 47.2%; Pred. No. 8.6e-127;
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nes 546; Conservative 175; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZETN; ZBG-GENRE-000831-1; pc.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR005483; Biotin_lipoyl.
InterPro; IPR005493; CPase_L_D2.
InterPro; IPR006991; HMGL-like.
InterPro; IPR000891; HMGL-like.
InterPro; IPR005919; PrC_OADA.
InterPro; IPR005930; Pyruv_carbox.
Pfam; PP00786; Biotin_lipoyl; I.
Pfam; PP00289; CPSase_L_chain; I.
PFam; PP00286; CPSase_L_chain; I.
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TIGREAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; AF295372; AAG37836.1; -.
HSSP; P24182; 1BNC.
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                                                                                                                                                                                                                                                                                                                                                                                     RVVVPAATKVEGGDLIVVV 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                         1127 QVHVKNGEPIQTGDLLLEI 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1043 PKIAEEFQVELERGKI-LHIKALALGDLNKSGQREVFFELNGQLRSVLVKDTAAMKEMHF 1101
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                                                                                    EVVRKMGDKVEARALAIKAGVPVVPGTDAPISCLQEAQEFAKTYDFPIIFKAAYGGGGRG 205
                                                                                                                                                                                                             358 NNGFRPDIGIITAYRSPGGAGVRLDGAAQL-GGEITAHFDSMLVKMICRGSDFETAVARA 416
                                                                                                                                                                                                                                                                                                                                                             SRGFQPDTGRIEVERSGEGMGIRLDSASAFQGAIISPHYDSLLVKVIASGKDLPTAATKM 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVLDLTGDKSRAVTAAKKAGLPVL-AESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRG 177
                                                                                                                     178 MRFVASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYER 237
                                                                                                                                                                                         DCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFI 297
                                                                                                                                                                                                                                                               EMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 AVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDP 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                595 WDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDV 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    655 SQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKD 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            715 MAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLS 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              774 GTTSQPSLSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGR--VY 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMTSQPSMGAIVACTKGTKLDTGISLDKVFDYSEYWEVARGLYAPFDCTATMKSGNADVY 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832 RHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLV 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      892 GAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEG--RSEGKAPLTE 949
                                                                                                                                           LADVIVNKPHGVRP-KDVAAPIDK-LPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 LGHVMVNGPMTPIPVKAKPSPVDPVIPSVSLGEPPLGFREVLLREGPEGFARAIRQHQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566 LLMDTTFRDAHOSLLATRVRTHDLKKIAPYVSHNFSNLFSLENWGGATFDAAMRFLSECP
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                                                                                                                                                                                                                                                                                                                                                                                                     417 QRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 AVRIGTEG -- SPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AYMIGKRGOYTPVGAYLAIDEIVKIALEHGVHLIHPGYGFLSENAEFARKVEQSGMVFVG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 PIPEVLDLIGDKSRAVIAAKKAGLPVLAESI-PSKNIDEIVKSAEGQIYPIFVKAVAGGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 STHT----SSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 SVHTRLRANSAIMQFQKILVANRGEIPIRIFRTAHELSLQTVAVYSHEDHLSMHRQKADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRGMRFVASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YERDCSLQRRHQXVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 1192;
                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus niger G.J.G., Van den Broeck H.C., Visser "Aspergillus niger pyruvate carboxylase.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR BOTIN (BY SIMILARITY).
EMBL, AJ009972; CAC19838.1;
-HSSP, P24182; LBNC.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR0016482; Biotin_attach.
InterPro; IPR0016482; Biotin_loyl.
InterPro; IPR001649; Biotin_loyl.
InterPro; IPR001649; CAPASE_L_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
43.4%; Score 2509.5; DB 3; Length
Best Local Similarity 46.7%; Pred. No. 3e-126;
Matches 546; Conservative 175; Mismatches 404; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1192 AA; 130866 MW; C7630C689BA23A64 CRC64;
                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Pyruvate carboxylase (EC 6.4.1.1).
                                                      PRT; 1192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR01235; pyruv_carbox; PROSITE; PS00188; atorin; 1. PROSITE; PS00866; CPSASE_1; 1. PROSITE; PS00867; CPSASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR003379; PYC_OADA.
InterPro; IPR005930; Pyruv_carbox.
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00384; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR005481; CPase_L_N. IPR000891; HMGL-like.
                                                                                                  (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00682; HMGL-like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYC_OADA;
                                                                                                                                                                                                                               niger.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biotin; Ligase
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-N400;
                                                                                                  01-MAR-2001
                                                                                                                                                                                                                          Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                      Q9HES8
RESULT 13
Q9HES8
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73 DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 ERAKSEAKAAFGSDEVYVEKLIENPKHIEVQILGDYEGNIVHLYERDCSVQRRHQKVVEV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLV--DEKGNHVFIEMNPRIQVEHTV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 TEEVTEVDLVKAQMRLAAGATL--KELGL-TQDKIKTHGAALQCRITTEDPNNGFRPDTG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 AAVNAGIPVIPGSDGPVDGLEDVVAFAEAHGYPIIIKAALGGGGRGMRFVRSKSEVKEAF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 APSVSLSDELRQRICEAAVQLMRSVGYVNAGTVEFLVSGDE---FYFIEVNPRIQVEHTI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL 72
                               pyruvate carboxylase.";

Gene 191.47-50(1997).

-! FUNCTION: PYRUVATE CARBOXYLASE CATALXZES A 2-STEP REACTION,

INVOLVING THE APP-DEPENDENT CARBOXXLATION OF THE COVALENTLY
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
GROUP TO PYRUVATE IN THE SECOND. CATALXZES THE INITIAL REACTIONS
OF GLOCOSE SYNTHESIS FROM PYRUVATE (BY SIMILARITY).

-! CATALXTIC ACTIVITY: ATP + PYRUVATE + HOO(3)(-) = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AAKKAGLPVLAEST-PSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding.
                                                                                                                                                                                                                              -!- PATHWAY: GLUCONEGGENESTS.
-!- SUBGNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBGLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SUBGLULAR TY: WITH OTHER BIOTIN CARBOXYLASES, PARTICULARLY FROM EUKARYOTES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOTIN CARBOXYLASE (BY SIMILARITY).
CARBOXYLITRANSFERASE (BY SIMILARITY).
BIOTIN CARBOXYL CARRIER PROTEIN
                stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             llarity 46.7%; Pred. No. 5e-126;
Conservative 182; Mismatches 397; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BIOTIN (BY SIMILARITY).
W; DFDZF003F838F591 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
ATP (BY SIMILARITY).
Kondo H., Kazuta Y., Saito A., Fuji K.-I.;
"Cloning and nucleotide sequence of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.3%; Score 2505;
                                                                                                                                                                                           ORTHOPHOSPHATE + OXALOACETATE.
                                                                                                                                                                                                                                                                                                                                                   EMBL, D83706; BAA12072.1; -.
HSSP; P24182; 1DV1.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005493; Biotin_lipoyl.
InterPro; IPR005491; CPase_LD2.
InterPro; IPR005401; CPase_LN.
InterPro; IPR005401; CPase_LN.
InterPro; IPR005909; PYC_OADA.
InterPro; IPR005909; PYC_OADA.
Ffam; PF00786; Biotin_carb_C; I.
Ffam; PF00786; Biotin_lipoyi: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF02786; CPSase_LD2; 1.
Pfam: PF0086; MGL-1ike; 1.
Pfam: PF00848; HMGL-1ike; 1.
TIGRFAMS: TIGR01235; PYLV-Carbox; 1
PROSITE; PS00188; BT0TIN; FALSE_NEG.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00866; CPSASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128336 MW;
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1112
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1112 111
1147 AA;
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1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 538;
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       985 KLDKRPGLYLEPLDLAKIKSQIRENYGAATEYDVA-----SYAMYPKVFEDYKKFVAK 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              989 FGNTSALDDREFFYGLVEGRETLIRLPDVRIPLLVRLDAISE-PDDKGMRNVVANVNGQI 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1038 FGDLSVLPTRYFLAKPEIGEEFHVELEKGKV-LILKLLAIGPLSEQTGQREVFYEVNGEV 1096
                                             EDPSKGFSPDTGKIEVYRSAGGNGVRLDGGNGFAGAIITPHYDSMLVKCTCRGSTYEIAR 446
                                                                                                                                                                                                                                                                                                                                       642
                                                                                             473
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                EDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQLGGE-ITAHFDSMLVKMTCRGSDFETAV 413
                                                                                                                                                                          LDYLADVIVN----KPHGVRPK---DVAAPI---DKLPNIKDLPLP--RGSRDRLKQLGPA 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIFRVFDALNDVDQLEVGIKAV-HAAEGVVEATICYSGDMLNPSKK-YNLPYYLDLVDKV 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              865 GLTGPDPEVYEHEIPGGQLTNLIFQASQLGLGQQWAETKKAYESANDLLGDVVKVTPTSK 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         925 VVGDLAQFMVSNKLTAEDVIARAGELDFPGSVLEFLEGLMGQPYGGFPEPLRSRALRDRR 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKVVRALVEFRIRGVKTNIPFLISLISHPVFVDGTCWTTFIDDTPELFALVGSQNRAQKL
                                                                                                                                                                                                                LAYLGDVAVNGSSIKGQIGEPKLKGDIIKPVLHDAAGKPLDVSVPATKGWKQILDSEGPE
                                                                                                                                                                                                                                                                                                                                                                      527 EDVAMRELYEDPWDRLRKLRKAVPNIPFQMLLRGANGVAYSSLPDNAIYHFCKQAKKCGV
                                                                                                                                                                                                                                                                                                                                                                                                                643 DIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 VKSGAHILAIKDMAGILRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADAVDGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           805 ADAVDAATDSLSGMTSQPSIGAILASLEGTEHDPGLNSAQVRALDTYWAQLRLLYSPFBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTPGPTGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  882 VVGDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-GKAP------LIEVPEEEQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRR
                                                                                                                                                                                                                                                       523 AFARDLREQDALAVIDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGAT
                                                                                                                                                                                                                                                                                   414 ARAQRALAEFTVSGVATNIGFLRALIREEDFTSKRIATGFIADHPHLLQAPPADDEQGRI
                                                                                                                                                                                                                                                                                                                                     YDVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB). Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEATITASVDGKIDRVVVPAATKVEGGDLI 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMVISAPHSGKVSSLLVKEGDSVDGQDLV 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K1041;
MEDLINE=97354293; PubMed=9210587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                               367 TITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV
                                                                           SGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVNKP
                                                                                                                                    542 RDAHQSLLATRVRIVDLVRAAEPSARLIPNLFSIEMWGGAIFDVAYRFLKEDPWDRLIKL
                                                                                                                                                                                                                                                                     AAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSL
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                                                                                                                                                                                                                                                                                                                                                                                       842 NLRAQATALGLADRFELLIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFA
                                                                                                                                                                                                                                                                                                                                                                                                   902 ADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDAD
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                                               RVFKTNIPFLENVVQHPKFLSGEYDTSFIDTTPELFVFPRRKDRGTKMLTYIGTVTVNGF
                                                                                                                                                                                                            REAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAI
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                                                                                                                       HGVRPKDVAAPI---DKLPNIKDL-PLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTF
                                                                                                                                                                 RDAHQSILLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDEL
                                                                                                                                                                                                                        Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Last annotation update)
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01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Adazer P., Frangeul L., Buchrisser C., Rusnick C., Amend A.,

Adazbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Bentian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Moueno E., Maltournam A., Mata Vicente J., Org. F., Perez-Diaz J.-C., Purcell R.,

A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simosa N., Tierrez A.,

A Remmel B., Rose M., Schlueter T., Simosa N., Tierrez A.,

Romand J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";

Strace 294:849-852(2001).

B. Exbi, Listilist; LWO01072:

InterPro; IPR005479; CPase_L.D.

R. InterPro; IPR00689; Biotin_lapyl.

InterPro; IPR00891; HMGL-like.

B. Riam, PP00289; CPasse_L.D.

R. Ffam, PP00289; CPasse_L.D.;

R. Ffam, PP00289; CPasse_L.D.;

R. Ffam, PP00289; CPasse_L.D.;

R. Ffam, PP00289; CPasse_L.D.;

R. Ffam, PP00436; HMGL-like; 1.

R. Ffam, PP00436; HMGL-like; 1.
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43.1%; Score 2493; DB 16;
Best Local Similarity 45.8%; Pred. No. 2.2e-125;
Matches 526; Conservative 185; Mismatches 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR01235; pyruv_carbox; PROSITE; PS00866; CPSASE_1; 1. PROSITE; PS00867; CPSASE_2; 1.
STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
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964 K------ERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLI 1012
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                                             604 AMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPALDA 663
                                                                                                                                                            602 QIPNVWFQMLLRGANAVGYKNYPDNVIREFVKQSAQSGVDVFRVFDSLNWIKGMFVSIDA 661
                                                                                                                                             664 VLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAA 723
                                                                                                                                                                                            724 VIKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSA 783
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Search completed: September 24, 2003, 15:59:16 Job time : 93.3413 secs

5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2003

- protein search, using sw model OM protein

September 24, 2003, 15:51:53; Search time 34.741 Seconds (without alignments) 3155.707 Million cell updates/sec Run on:

US-09-974-973A-19 Perfect score:

5788 1 MSTHTSSTLPAFKKILVANR.....RVVVPAAIKVEGGDLIVVVS 1140 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

PIR_76:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	pyruvate carboxyla pyruvate carboxylas pyruvate carboxylase biotin carboxylase	
SUMMARIES	D70671 A47255 A87255 A83918 F69685 F69685 AH12208 AH12208 AB2911 AB2911 AB2911 AB2913 AB2913 AB331 AB4608 AB460	
DB		
ŭ	11127 11128 11128 11149 11149 11140 11140 11150 11175 11180 11195	
ery	4.844444444444444444444444444444444444	
Score		
Result No.		

probable pyruvate	hypothetical prote	nypouleuran proce	biotin carboxylase	hypothetical prote	hypothetical prote	biotin carboxylase	biotin carboxylase	biotin carboxylase	biotin carboxylase	acetyl-CoA carboxy	biotin carboxylase	biotin carboxylase	acetyl-CoA carboxy	acetyl-CoA carboxy	biotin carboxylase	
B83471	D87647	D0/04/	B97338	AC2997	F98286	C70444	AI0912	B86722	AD0445	T07093	T44813	F64105	C95049	A69581	A97920	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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16.9		2.91	10.0		16.6	16.5	16.5		16.4	16.4	16.3	16.3	16.3	16.3		(

ALIGNMENTS

RESULT 1

D70671 pyruvate carboxylase (EC 6.4.1.1) - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2002 C;Accession: D70671; S73055 R;COle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Daviss, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
--

Nature 393, 537-544, 1998

AAAthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Aithers Deciphering the biology of Mycobacterium tuberculosis from the complete genc
A; Reference number: A70500; MuID: 98295987; PMID: 9634230
A; Accession: D70671
A; Accession: D70671
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-1127 <COL>
A; Across-references: GE: 283018; GB: AL123456; NID: 93261671; PIDN: CAB05410.1; PID: 916948
A; Experimental source: strain H37Rv
A; Experiment

A. MCLOSALLE TYPE: DNA
A. RESIGUES: 1-353, 'TRAGSARCDPPAVPVSAWTAAPTWRRNQPVLRLHAGQADLS',396-1115, 'EWRAETCWWW' <
A. CTOSE TE TETETENCES: EMBL: U00024; NID: 9560506; PIDN: AAA50948.1; PID: 9560527
C. Genetics: Pos; Pyc
A. Gene: pos; Pyc
C. Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindic; Keywords: biotin binding; ligase; mitochondrion
F: 4-457/Domain: biotin carboxylase homology <BCH>
F: 4-457/Domain: biotin carboxylase homology <BCH>
F: 1055-1127/Domain: lipoyl/biotin-binding homology <ALPB>
F: 1093/Binding site: biotin (Lys) (covalent) #status predicted

Length 1127; DB 2; Query Match 64.1%; Score 3712.5; DB 2. Best Local Similarity 64.4%; Pred. No. 3.4e-196; Matches 730; Conservative 153; Mismatches 239;

12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY 71 61 11; Indels qq

72 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131 132 TAAKKAGLPVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKLA 191 οy QQ δ

122 AAAREAGLPVLMSSAPSASVDELLSVAAGMPFPLFVKAVAGGGGGRGMRRVGDIAALPEAI 181

g

242 3 3 2 2 2 3 3 3 2 2 2 3 3 3 2 2 2 2 2
4 4 4 5 5 5 5 5 6 7 7 7 7 8 8 5 8 5 6 6 0 0 0

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A47255

Pyruvate carboxylase (EC 6.4.1.1) precursor [similarity] - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Feb-2002
C;Accession: A47255
R;Zhang, J; Xia, W.L.; Brew, K.; Ahmad, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 1766-1770, 1993
```

A;Title: Adipose pyruvate carboxylase: amino acid sequence and domain structure deduc A;Reference number: A47255; MUID:93189578; PMID:8446588
A;Accession: A47255; MUID:93189578; PMID:8446588
A;Accession: A47255
A;Accession: A47255
A;Molecule type: mRNA
A;Residues: 1-1178 < CHA>
A;Residues: 1-1178 < CHA>
A;Residues: 1-1178 < CHA>
A;Residues: GB:103192; NID:9293743; PIDN:AAA39737.1; PID:9293744
A;Resperimental source: 373-41 adipocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:126874, NCBIP:126875)
C;Superfamily: pyruvate carboxylase; biotin arboxylase homology; lipoyl/biotin-bindic; Reywords: biotin binding: liqase; mitochondrion #status predicted <TRP>
F;1-20/Domain: transit peptide (mitochondrion) #status predicted <TRP>
F;3-494/Domain: biotin carboxylase #status predicted <MAT>
F;3-494/Domain: biotin carboxylase homology <ALB>
F;1105-1178/Domain: lipoyl/biotin-binding homology <ALB>
F;1144/Binding site: biotin (Lys) (covalent) #status predicted DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 132 158 IAIAAGVPVVPGTDSPISSLHEAHEFSNTFGFPIIFKAAYGGGGRGMRVVHSYEELEENY 217 192 TEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVEI 251 252 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 311 372 RSPGGAGVRIDGAAQL-GGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 430 491 KDVA-APID-KLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTFRDAHQSL 548 - GVVEAAISYTGDVADPSRTKYSLEYYNGLAEELVRAGTHILCIKDMAGLIKPAACTMLV 756 SSLRDRFPDLPLHIHTHTHDTSGAGVAAMLACAQAGADVVDVAVDSWSGMTSQPSWGALVAC 816 133 AAKKAGLPVL-AESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKLA 191 312 EVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 371 431 NIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVNKPHGVRP 490 549 LATRVRSFALKPAAEAVAKLIPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNV 608 609 NIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETN 668 TAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLV 728 TALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSAIVAA 787 13 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL 72 17; Gaps Query Match 43.9%; Score 2541.5; DB 1; Length 1178; Best Local Similarity 47.0%; Pred. No. 9.4e-132; Matches 537; Conservative 187; Mismatches 401; Indels 17; 458 757 218 ð a qq ŏ qα ΟŽ qq q QΥ q QΥ QQ QΫ q δ q qq g ò ð Q_{λ} ă δ qq δy

12;

48

108

167

227

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74 QMHRQKADEAYLIGRGLAPVQAYLHIPDIIKVAKENGVDAVHPGYGFLSERADFAQACQD 1333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDFNEKLYTLDYYLKMAEEIVK 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           674 FRIFDSLNYLPNMLLGMEAAGSAG-GVVEAAISYTGDVADPSRTKYSLEYYMGLAEELVR 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               793 VVDVAVDSMSGMTSQPSMGALVACTKGTPLDTEVPLERVFDXSEYWEGARGLYAAFDCTA 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  853 TMKSGNSDVYENEIPGGQYTNLHFQAHSMGLGSKFKEVKKAYVEANQMLGDLIKVTPSSK 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                824 PGPTGR--VYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSK 881
                                                                                                                                                                                                                                LGVRRSSTAPVASPNVRRLEYKPIKKVMVANRGEIAIRVFRACTELGIRTVAVYSEQDTG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EGRSEGKAPLTEVPEEEQAHLDA-DDSKERRNSLNRLLFPKPTEEFLEHRRFGNTSA 994
                                                                                                                                                                                                                                                                                                                                                                                   NGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVL-AESTPSKNIDEIVKSAEGQTYPIFV
                                                                                                                                                                                                                                                                                                                                                                                                                  -----FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRG
                                                                                                                                                                                                                                                                                  SFHRSFASEAVRIGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAVAGGGGRGMRFVASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDFETAVARAORALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLOAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 KDHPTAATKMSRALABFRVRGVKTNIPFLQNVLNNQQFLAGIVDTQFIDENPELFQLRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDEQGRILDYLADVTVNKPHGVRPKDVA-APIDKL-PNIKDLPLPRGSRDRLKQLGPAAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        525 ARDLREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585 VAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGAHILAIKDMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  764 AVDGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGT
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                                                                                                                                  Gaps
       F;1105-1178/Domain: lipoyl/biotin-binding homology <LPB>
F;1144/Binding site: biotin (Lys) (covalent) #status experimental
                                                                                                                                410; Indels
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                                                                                 DB 2;
                                                                         Score 2539.5; DB 2,
Pred. No. 1.2e-131;
15; Mismatches 410;
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                                                                                                                                Conservative 185;
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                                                                                                     Similarity
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Matches
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C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C;Reywords: biotin binding; gluconeogenesis; homotetramer; ligase; mitochondrion
E;1-20/Domain: transit peptide (mitochondrion) #status predicted <TNP>
E;21-1178/Product: pyruvate carboxylase #status predicted <MAI>
E;39-494/Domain: biotin carboxylase homology <BCH>
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                                                                                                                                                                                                                                                                                                                                         997 RHGEEVTPEDVLSAAMYPDVFAQFKDFTATFGPLDSLNTRLFLQGPKIAEEFEVELERGK 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1079 FAG-VVTVTVAEGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIV 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Rattus norvegicus (Norway rat)
C; Date: 20-Jan-1996 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2002
C; Accession: S68252; S7393; JC4391; S06440
R; Jitrapakdee, S.; Booker, G.W.; Cassady, A.I.; Wallace, J.C.
Biochem. J. 316, 631-637, 1996
A; Title: Cloning, sequencing and expression of rat liver pyruvate carboxylase.
A; Reference number: S68252; MUID:96257760; PMID:8687410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-1178 <JIT1>
A;Cross-references: EMBL:U36585; NID:91040973; PIDN:AAC52668.1; PID:91040974
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                                                                                                                                  FAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGR--VYRHEIPGGQLSNLRA
                                                 TKGTPLDTEVPLERVFDYSEYWEGARGLYAAFDCTATMKSGNSDVYENEIPGGQYTNLHF
                                                                                                                                                                                                 KYDIPDSVIAFLRGELGNPPGGWPEPLRTRAL-----EGRSECKAPLTEVPEEEQAHLD
                                                                                                                                                                                                                                                937 ELSFPRSVVEFLQGYIGIPHGGFPEPFRSKVLKDLPRIEGRPGASLPPLNLKELEKDLID
                                                                                                QATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQ
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A; Residues: 489-505 <JII2>
A; Residues: 489-505 <JII2>
A; Experimental source: liver
B; Lehn, D.A.; Moran, S.M.; MacDonald, M.J.
Gene 165, 331-332, 1995
A; Title: The sequence of the rat pyruvate carboxylase-encoding cDNA.
A; Reference number: JC4391; MUID:96096548; PMID:8522203
A; Accession: JC4391
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-21, FP, 223-865, D', 867-976, G', 978-1178 <LEH>
A; Cross references: GB:032314; NID:9929987; PIDN:AAA96256.1; PID:9929988
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Arch. Biochem. Blophys. 266, 270-276, 1988
A)Title: A rapid purification method for rat liver pyruvate carboxylase A; Reference number: S06440; MUID:89024676; PMID:3178228
A; Accession: S06440
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyruvate carboxylase (EC 6.4.1.1) precursor - rat
C:Species: Rattus norvegious (Norway rat)
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qq	973 RIEGRPGASLPPLNLKELEKDLIDRHGEEVTPEDVLSAAMYPDVFAQFKDFTATFGPLDS 1032	qq	484 GYPGLE-KTKKPVFDKPPVPKLKLSEPIPDGTKQILDQHGPEGLAKWVKEQKHVLTDTT 542
Qy Db	995 LDDREFFYGLVEGRETLIRLDDVRTPLLVRLDAISEPDDKGMRNVVANVAQIRPMRVRD 1054	QY	541 FRDAHQSLIATRYRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDKLDE 600
Qy		Qy Db	LREAMPNVIOMLERGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIEDALNDVSQMRPA
QY Db	1114 SVDGKIDRVVVPAATKVEGGDLIVVV 1139 	QY Db	661 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKNAEEIVKSGAHILAIKDMAGILR 720
RESULT A83978 Pyruvat	4 ge carboxylase pycA [imported] - Bacillus halodurans (strain C-125)	Oy QU	PAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTISQPS
C;Speci C;Date: C;Acces R;Takam	C;Species: Bacillus halodurans C;Aacesslon: A89378 B;Takami, H.; Nakasone, K.; Takaki, Y.: Maeno, G.: Sasaki, R.: Masui, N.: Puit, F. Hira	Qy Db	781 LSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGIPGPTGRVYRHEIPGGGL 840 ::: :: ::
Nucleic A;Title A;Refer A;Acces	3, 4317-4331, 2000 nome sequence of the alkaliphilic bacterium Bacillus halodurans 183650; MUID:20512582; PMID:11058132	oy Db	841 SNLRAQATALGIADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF 900
A; Statu A; Molec A; Resid	SIO> SEADONISTE, CE-BROOMON, WITH LATER OF THE WATER OF T	Qy Db	901 AADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEDAHLDA 960 :
A; Exper C; Genet A; Gene: C; Super	N. Story Laterians: Grantonia, GB. BANGOLOGA; NID: 9101/5192; FIDN: BABGOS44.1; GSFDB: GNUU A; Experimental source: Strain C-125 A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Grantonians A; Genetics: A; Garbovviase: biotin osthownians bomologus A; Grantonians A; Gran	QY Db	961 DDSKER-RNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRE 1009 :
Query Best Match	43.6%; Score 2525.5; DB 2; tty 46.8%; Pred. No. 6.9e-131; Servative 185; Mismatches 400;	Oy Dp	1010 TLIRLPDVRTPLLVKLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADS 1069 ::: : :
oy oy	AALETGAATVALYPREDRGSPHRSFASEAVRICTEGSPV 6	QY Db	1070 SNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAAT 1128
AQ Q		Qy	1129 KVEGGDLIVVV 1139 :: : 1137 AIQTGDLLEV 1147
Qy	129 RAVTAAKKAGLPVLAEST-PSKNIDEIVKSAEGQTYPIFVKAVAGGGRGMRFVASPDEL 187 	RESULT 5 F69685 Pyruvate	carboxylase (EC 6.4.1.1) pych [similarity] - Bacillus subtilis
Qy Dp	188 RKLATEASREABAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQK 247 ::	C;Specie C;Date: C;Access R;Kunst,	s: Bacillus subtilis 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Aug-2000 ion: F69685 F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
Cy Op	248 UVEIAPAQHLDPELRDRICADAVRFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEH 307	C.; Bron A.; Ehrl Nature 3 A;Author	, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; lch, S.D.; Emmerson, P.T.: Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, 90, 249-256, 1997 s: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
Qy Db	308 TVTEEVIEVDLVKAQMRLAAGATLKELGL-TQDKIKTHGAALQCRITTEDPNNGFRPD 364	<pre>iech, J. Koetter, A;Author Y, M.; O</pre>	lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Qy Dp	365 TGTITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEF 423	Rieger, A; Author akeuchi, T.; Wint	M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl st. Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya ers, P.; Wipat, A.; Yamamoto, H.; Tamane, K.; Yasumoto, K.; Yata, K.; Yoshida
Oy Dp	424 TVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVN 483 1	A; Author A; Title: A; Refere A; Access	A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Reference number: A69580; MUID:98044033; PMID:9384377 A;Accession: F69685
γo	484 KPHGVRPKDVAAPIDKLPNIK-DLPLPRGSRDRLKQLGPAAFARDLREGDALAVTDTT 540	A; Status A; Molecu A; Residu	: preliminary; nucleic acid sequence not shown; translation not shown le type: DNA es: 1-1148 <kun></kun>

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A;Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13359.1; PID:g2633857 A;Experimental source: strain 168
A;Experimental source: strain 168
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genes: pycA
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding F;Reyworks: ligase
F;Reyworks: ligase
F;ReyGomain: biotin carboxylase homology <BCH>
F;1073-1146/Domain: lipoyl/biotin-binding homology <LPB>
F;1112/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                     YLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRA 130
                                                                                                                                                                                                                                                                                                                        VTAAKKAGLPVLAEST-PSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                      LATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVV 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVN-- 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKA 70
                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 TEEVTEVDLVKAQMRLAAGATL--KELGLIQDK-IKTHGAALQCRITTEDPNNGFRPDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 TITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: || || : : | | : : | || RGIKTNIPFLENVAKHEKFLTGQYDTSFIDTTPELFNFPKQKDRGTKMLTYIGNVTVNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 PGIGKKEKPAFDKPLGVKVDVDQQP-----ARGTKQILDEKGAEGLANWVKEQKSVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQ
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                                                                                                                                                                                                         48;
                                                                                                                                                                     Length 1148;
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                                                                                                                                                           Query Match
Best Local Similarity 46.0%; Pred. No. 0.05. 392;
Matches 533; Conservative 186; Mismatches 392;
                                                                                                                                                                                                                                                                                                                                                                     131
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A; Accession: JC2460
A; Molecule type: mRNA
A; Recassion: JC244, WPV, 227-351, A', 353-384, PT', 387-485, DV', 488-637, R', 639-728, A',
A; Residues: 1-224, WPV, 227-351, A', 353-384, PT', 387-485, DV', 488-637, R', 639-728, A',
A; Cross-references: GB:S72370; NID:873807; PIDN:AAB31500.1; PID:9632808
B; Lamhonwah, A.M.; Quan, F.; Gravel, R.A.
Arch. Biochem: Biophys. 254, 631-636, 1987
A; Title: Sequence homology around the biotin-binding site of human propionyl-CoA carb
A; Reference number: A27883; MUID:87212051; PMID:3555348
A; Accession: B27883
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A;Cross-references: GB:M26122; NID:g189657; PIDN:AAA36423.1; PID:g387003
B;Freytag, S.O.; Collier, K.J.
J. Biol. Chem. 259, 12831-12837, 1984
A;Title: Molecular cloning of a cDNA for human pyruvate carboxylase. Structural relat A;Reference number: S01469; MUID:85030380; PMID:6548474
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A;Map position: 11q11-11q13.1
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi c;Superfamily: pyruvate carboxylase; ligase; mitochondrion
C;Superfamily: pyruvate carboxylase #status predicted <TNP>
F;1-20/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;21-1178/Product: pyruvate carboxylase #status predicted <MAT>
F;31-494/Domain: biotin carboxylase homology <LDB>
F;1105-1178/Domain: lipoyl/biotin-binding homology <LDB>
F;1144/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                   1062 ATAEKADSSNKGHVAAPFAGVVTVTVAE-GDEVKAGDAVAIIEAMKMEATITASVDGKID 1120
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                                                                                                                                                                                                                                                                                                                                              1002 YGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVT 1061
                                                                                                                                                                             -EQAHLDADDSKERRNSINRLLFPKPTEEFLEHRRRFGNTSALDDREFF 1001
                                                     EKDVYEKGESLDFPDSVVELFKGNIGQPHGGFPEKLQKLILKGQE----PITVRPGELLE 951
PADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEE--- 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyruvate carboxylase (EC 6.4.1.1) precursor - human NiAlternate names: pyruvate:carbon dioxide ligase (ADP-forming) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 18-Aug-2000 #text_change 01-Feb-2002 C;Accession: G01933; JC2460; B27883; S01469 R;Walker, M.E.; Jitrapakdee, S.; Val, D.L.; Wallace, J.C. A;Reference number: H00708
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C;Genetics:
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A; Status: translated from GB/EMBL/DDBJ
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1135-1178 <FRE>
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A; Residues: 1083-1178 <LAM>
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A; Residues: 1-1178 <WAL>
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pyruvate carboxylase homolog pycA [imported] - Listeria monocytogenes (strain EGD-e) C; Species: Listeria monocytogenes C; Date: 27-Nov-2001 #text_change 14-Dec-2001 C; Accession: AH1208 C; Accession: AH1208 C; Accession: AH1208 C; Duchaud, E.; Durand, A.; Baquero, F.; Berche, P.; Bioec.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Althe: Comparative genomics of Listeria species. Asitle: Asitle: Comparative Genomics of Listeria Species. Asitle: Comparative Genomics of Comparative Genomics G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1146 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99150.1; PID:g16410474; GSPDB:GN00177
                                            1038 FLGGPKIAEEFEVELERGKT-LHIKALAVSDLNRAGOROVFFELNGOLRSILVKDTQAMK 1096
                                                                                                                                                                                                 1000 FFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVES 1059
                                                                                                                                                     1060 VTATAEKADSSNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGK 11118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 EVTEVDLVKAQMRLAAGATLKELGLT---QDKIKTHGAALQCRITTEDPNNGFRPDTGTI 368
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12 FKKILVANRGEIAVRAPRAALETGAATVAIYPREDRGSFHRSFASBAVRIGTEGSPVKAY 71	191 ATEASREARAPGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250 185 CRSAKSEAKRAPGIEDIFIEKYLEGPKHIEVQVLGDKYGNIVHLYERDCSYQRRHQKVVE 244 251 IAPAQHLDPELRDINICADAKECRSIGYQGAGTVEFLVDEKGNIVHLYERDKYVEF 244 252 IAPAQHLDPELRDRICADAKECRSIGYQGAGTVEFLVDEKGNIVPTEMNPRIQVEHTVT 310 245 LITPAVSMSEEKRLEICEDALKIARSIGYRSAGTLEFLLDKHGNINFRIQVEHTIT 304 311 EEVTEVDLVKAQMRLAGGATLK-1-TQDKIKTHGAALQCRITTEDPNNGFRPDTGT 367	05 EMVTGIDIVQSQILIAEGYKLNSPEVGINSQEDIHVNGYALQCRITTEDPSNSFAPDTGR 68 ITAYRSPGGAGVRLDGA-AQLGGEITAHFDSMIVKMTCRGSDFETAVARAQRALAEFTVS	48. GVARANOAR DALPNIKDELPRGSRDKLKOLGFAAFARDEQDA-AVIDTERDA 544 485 GHKIEVDVPSVPKYEIKE-PL-RGTKQILDEKGPKGLVEWIKDQDKLLITDTTMRDA 539 545 HQSILATRVRSFALKPAAEAVAKITPELLSVEANGGATYDVAMFFLFEDPWDRLDELREA 604 [111:111:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1	660 LNQG-KVAEACMCYTGDILDTNRDKYTLNYYNLAKEIEKSGAHILGIKDMSALLKPYAA 718 725 TKLVTALRREDLPVHYHTHDTAGGOLATYFAAAQAGADAVDGASAPLSGTTSQPSLSAI 784 11: 11: 1: 1: 1: 1 1 1 1 1 1 1 1 1 1 1 1 1	905 QKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADDSK 964 : : : : :
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OY 488 VRPKDVAAPIDKLENIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTFRD 543 ::: : : : : :	72 78 78 84	QY 844 RAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAAD 903 1 1 1 1 1 1 1 1 1 1	Db 957 KAELKEKMGYEPTEKDVISYILININININININININININININININININININI	RESULT 8 D97227 PYTUVATE Carboxylase, PYKA [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Accession: D97227 R; Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R; Lee, J. Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J; Bacteriol. 183, 4823-4838, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo	A; Accession: D9/22/ A; Accession: D9/22/ A; Accession: D9/22/ A; Molecule type: DNA A; Residues: 1-1144 <kur> A; Cross-references: GB: AE001437; PIDN: AAK80607.1; PID: g15025689; GSPDB: GN00168 A; Experimental source: Clostridium acetobutylicum ATCC824 C; Genetics: A; Gene: CAC2660 C; Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding Query Match 43.0%; Score 2491.5; DB 2; Length 1144; Beet Local Similarity 45.3%; Pred. No. 5e-129; Matches 520; Conservative 204; Mismatches 391; Indels 33; Gaps 14;</kur>

QY 1071 NKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATK 1129 :	QY 544 AHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELKE 603
Qy 1130 VEGGDLIV 1137 : : Db 1134 VOSGQLIV 1141	QY 604 AMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDA 663
RESULT 9 AC1565 C:Decies: Listeria innocua (strain Clipl1262) C:Species: Listeria innocua (strain Clipl1262) C:Species: Listeria innocua C:Decies:	Qy 664 VLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKNABEIVYSGAHILAIKDMAGLLRPAA 723 1 1 1 1 1 1 1 1 1
0.9 1.33 AAKKAGLPVLAEST-PSKNIDEIVKSAEGGTYPIFVKAVAGGGGGRGNEYASPDEIRKLA 191 1.1 1 1.1	RESULT 10 G89881 C:Species: Staphylococcus aureus C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001 C:Accession: G89881 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Recession: G89881 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1150 <kur> A;Coss-references: GB:BAQ00018; PID:g13700915; PIDN:BAB42211.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Genetics: A;Gene</kur>

KKLLVANRGEIAIRIFRAAAELDISTVAIYSNEDKSSLHRYKADESYLVGSDLGPAESYL 64	DIDBIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 132 : : : :	AAKKAGLPVL-AESTPSKNIDEIVKSAEGQIYPIFVKAVAGGGGRGMRFVASPDELRKLA 191 	188	TEASREABAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVEI 251 	APAQHLDPELRDRICADAVKFCRSIGYQGAGTVBFLVDEKGNHVFIEMNPRIQVEHTV 309 : :: APSVGLSPTLRQRICDAAIQLMENIKYVNAGTVEFLVSGDEFFFIEVNPRVQVEHTI 301	m	30		GVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEGGRILDYLADVTVNKP 485 :: : : : GVRINTPFI.IDFT.IDFT.IDFT.IDFT.IDFT.IDFT.IDFT.ID	TIME THE THE THE CHONGING THE THE TRUNKTIN . # 1		LREODALAVTDTTERDAHOSLLATRVRSFALKPAAEAVAKLIPELLSVEAWGGATYDVAM 587	ODVILTOTIFRDAHQSILATRVRTKOMINIASKTADVFKDGFSLEMWGGATFDVAY 586	RFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGYDIFRI 647 - - - - - - - - - - - -	FDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDP-NEKLYTLDYYLKMAEEIVKSG 706	JMWVDQMKVANDAVQEAG-KISEGTICYTGDILNPERSNIYTLEYYVKLAKELEREG 705	AHILAIKDMAGLIRPAAVTKLVTALRREFDLPVHVHTHDIAGGQLATYFAAAQAGADAVD 766 	GASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGP 826	NSWSGLTSQPSANSLYXALNGFPRHLRTDIEGMESLSHYWSTVRTYYSDFESDIKSP 825	TGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDL 886 	VGAGVDPADFAADPOKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAP 946	ALYMVQNDLDEQSVITDGYKLDFPESVVSFFKGEIGQPVNGFNKDLQAVILKGQEA 941	EVPEEQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRFGNTSAL 995	RPGEYLEPVDFEKVRELLEEEQQGPVTEQDIISYVLYPKVYEQYIQTRNQYGNLSLL 1001	EFFYGLVEGRETLIRLPDVRIPLLVRLDAISEPDDKGMRNYVANVNGQIRPMRVRDR 1055	111	: : NVHTNANVKPKADKSNPSHIGAQMPGSVTEVKVSVGETVKANQPLLITEAMKMETTIQAP 1120
KKLLVAN	DIDEIIG: :1: NIERIID	AAKKAGLI 	TAIKADL	TEASREAD 	APAQHLDI : APSVGLSI	TEEVTEVI	TEMVIGI	TITAYRS	SGVATNIC	HGVRPKD		LREQDAL	VKKQDDV	RFLFEDPY : NFLKENPY	FDALNDVS	FDSLNWVI	AHILAIKI FHILAIKI	GASAPLS	TAVASMS(TGRVYRHI : : NTEIYQHI	ALHLVGAC	ALYMVQNI	LTEVPEE	ď	DDREFFY(: DTPTFFF	SVESVTA	: I : NVHTNAN
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C;Accession: AE2911
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
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                                                                                                                                                                                                                                                                                                                                                                          ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AE2911
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1174 <KUR>
A,Cross-references: GB:AE008688; PIDN:AAL43707.1; PID:g17741236; GSPDB:GN00186
                                                                                                                                                               pyruvate carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 AKDMGPIESYLSIEEVIRVAKLSGADAIHPGYGLLSESPEFVEACNKAGITFIGPTPDTM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 -TEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPRIQVEHTVTEEVTEVDLVKAQMRLAAGATL -- KELGL -TQDKIKTHGAALQCRITTED 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 AQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILD 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 QDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFL 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 TLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIG---- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 IRKKEDLAREVTEAKREAKAAFGKDEVYLEKLVERARHVESQILGDTHGNVVHLFERDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VASPDELRKLATEASREAEAAFGDGAVYVERAVINPOHIEVQILGDHTGEVVHLYERDCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 46.6%; Fred. No. J.rello.
Matches 541; Conservative 173; Mismatches 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.7%; Score 2473.5; DB 2
46.6%; Pred. No. 5.1e-128;
                             1115 VDGKIDRVVVPAATKVEGGDLIVVV 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain C58 (Dupont)
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A;Map position: circular chromosome
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AKDMGPIESYLSIEEVIRVAKLSGADALHPGYGLLSESPEFVEAUNKAGITFIGPTPDTM 13 DLTGDKSRAVTAAKKAGLPVLAESTP-SKNIDBIVKSAEQCTYPIFVKAVAGGGGRGMRF 18	320 NPRIQVEHTVTEVVTGIDIVKAQIHILEGAAIGTAESGVPKQEDIRLNGHALQCRITTED 379 357 PNNGFRPDTGTITAYRSPGGAGVRLD-GAAQLGGEITAHPDSMLVKMTCRGSDFETAVAR 415	TEDPWERLSLIREGAPNILLLQMLLRGANGYGYKNYPDNVKIFVKGAARGGVDLFKVEDC OF TEDPWERLSLIREGAPNILLLQMLLRGANGYGYKNYPDNVKIFVKGAARGGVDLFKVEDC OF THE STATE OF THE STA	1058 ESYTATABKADSSNKGHVAAPFAGVYT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVD 1116
4 6 4 6 4 6			da do
Db 557 EKRYLVTDTTMRDGHQSLLATRVRTHDIARVASVYSKALPQLLSLECWGGATFDVSWRFL 616 591 FEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDA 650 1	831 856 891 916 972 972 999 1031	Oy 1117 GKIDRVVVPAATKVEGDLIV 1137 Db 1150 GKIAEVLVKPGDDIAKDLLI 1170 RESULT 12 C97686 Pyruvate carboxylase (U51439) [imported] - Agrobacterium tunmefaciens (strain C58, Cereor C; Species: Agrobacterium tunmefaciens C; Accession: C97686 Pyruvate carboxylase (U51439) [imported] - Agrobacterium tunmefaciens (strain C58, Cereor C; Species: Agrobacterium tunmefaciens C; Accession: C97686 C; Accession: C97686 A; Title: Ganome Sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Accession: C97686 A; Title: Ganome Sequence of the Plant Pathogen and Blotechnology Agent Agrobacterium tunmers A; Accession: C97686 A; Title: Ganome Sequence of the Plant Pathogen and Blotechnology Agent Agrobacterium tunmers A; Accession: C97686 A; Acc	PAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIG 62

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A;Introns: 34/3; 103/3; 246/1; 451/3; 567/2; 821/1; 1045/3; 1126/3
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi
C;Keywords: ligase
F;1140/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                   955 QAHLDA-----DDSKERRNS----LNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLV 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963 AADLDAERKSFEDSVGRKLSDQEFASALMYPKVFTDYATAHETYGPTSVLPTPVYFYGLK 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1023 PEEEVEYDLERGKTLVIVN-QAMSETDEKGMVTVFFELNGQPRRIKVPNRAKGASGGVRR 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyruvate carboxylase (EC 6.4.1.1) D2023.2 [similarity] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1066 KADSSNKGHVAAPFAGVV-TVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVV 1124
                                                                                                                                                                                                                                                                                            954
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:281052; PIDN:CAB02872.1; GSPDB:GN00023; CESP:D2023.2 A;Experimental source: clone D2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C;Accession: T20346
R;Kershaw, J.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219260
                                                  || ::||||| | : | |: |:||| | 668 MRVSMDAVLEEN-KLCEAAICYTGDILNPDRAKYDLNYYNLAKEVEKAGAHIIAVKDMA
                                                                                                                                   SQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1006 EGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAE
                           657 MRPAIDAVLEINTAVAEVAMAYSGDLSDPNEKLYILDYYLKMAEEIVKSGAHILAIKDMA
                                                                                                         GLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTT
                                                                                                                                                                                                                                SQPCLGSIVEALHGSERDSGLDPDLIRRISFYWEAVRHQYAAFESDLKGPASEVYLHEMP
                                                                                                                                                                                                                                                                      GGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVD
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Best Local Similarity 45.2%; Pred. No. 1./e 2...
Matches 523; Conservative 200; Mismatches 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A.Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
                                                                                                 Pyruvate carboxylase (EC 6.4.1.1) [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVVEIAPAQHIDPELRDRICADAVKFCRSIGYQGAGTVEFLVD-EKGNHVFIEMNPRIQV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHTVTEEVTEVDLVKAQMRLAAGATL--KELGL-TQDKIKTHGAALQCRITTEDPNNGFR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EHTVTEEVTGIDIVKAQIHILEGFALGTPESGVPRQEDIRLNGHALQCRITTEDPEQNFI 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDYGRIQAYRSAAGFGIRLDGGTAYSGAFITRYYDPLLVKVTASGATPLEAIHRMDRALR 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 KILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIG-----TEGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.6%; Score 2464.5; DB 2;
46.6%; Pred. No. 1.6e-127;
Live 171; Mismatches 408;
  GKIAEVLVKPGDQIDAKDLLI 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 171;
                                                                                                                                                                                                                                                                                                                                            A:Residues: 1-1158 <KUR>
A:RCOSS-references: GB:AE008917; P
A:Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 538; Conserv
                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                         A: Molecule type: DNA
                                                                                                                                                              C; Accession: AE3285
                                                                                                                                                                                                                                                                                 A; Accession: AE3285
A; Status: preliminar
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C; Superfamilw.
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2 TAAKKAGLPVLAEST-PSKNIDEIVKSAEGGTYPIFVKAVAGGGGRGMRFVASPDELRKL 190 : :	1. ATEASREABAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250 2. FRRSYSEAQAAFGDGSLFVEKFVERPRHIEVQLLGDHHGNIVHLYERCSVORRHOKVVE 271	IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 31		1 YRSPGGAGVRLDGAAQLGGE-ITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVA 429 	0 TNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVNKP 485	6 -HGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTFRDA 544 	5 HQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREA 604 	5 MPNVNIQMLLRGRNTVGYTPYPDSVCRAEVKEAASSGVDIFRIFDALNDVSQMRPAIDAV 664	5 LETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAV 724 	5 TKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSA 783 	4 IVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLS 841	2 NLRAQATALGIADRFELIEDNYAAVNEMLGRPTKYTPSSKVVGDLALHLVGAGV 895 	6 DPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEE 953 1 1 1 1 1 1 1 1 1	4 EQAHLDADDSKERRNSLNRILFPKPTEEFLEHRRRFGNTSALDDREFFY 1002 1	3 GLVEGRETLIRLPDVRTPLIVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDKSVESVTA 1062 	3 TAEKADSSNKGHVAAPFAG-VVIVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDR 1121 : : : : : : : : : : : :	2 VVV : 6 IHA
				> · · [4	30	٠ ﴿			65 LE 90 GK	25 49	784 IVA 809 IVA	842 NLR : 869 NLQ	96	54 EQA 77 NAK	e r	63 TAE 96 TRP	22 VVV : 56 IHA
Qy 1 Db	Qy 1	QY 2	Qy 3 Db 3	Qy 3	Oy 4	Qy 4	Qy 5 Db 5	QY 6 Db 6	Qy 6	Qy 7 Db 7	2y 7 Db 8	9 40 Db 8	Oy 8 DD	QY 9 Db 9	Oy 100 Db 103	Qy 10 Db 10	Qy 11 Db 11

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A. Accession: $6406
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Creations: 1-1178 CFED-
A. Cross-references: Expan $288.
A. Cross-references: Expan $288.
B. Elim, F.; Morris, C.P.; Occhiodoro, F.; Wallace, J.C.
J. Biol. Chem. 263, 11493-11497, 1988
A. Pitie. Sequence and domain structure of yeast pyruvate carboxylase.
A. Reference number: A92662; MUID:88298805; PMID:3042770
A. Accession: A29233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 1-461,'G',463-492,'D',494-594,'A',596-618,'Q',620-663,'S',665-771,'R',773
A,Cross-references: EMBL:J03889; NID:g172101; PIDN:AAA34843.1; PID:g172102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cymperfamily: pyruvate carboxylase; biotin carboxylase homology; lippyl/blotin-bindi C;Reywords: biotin binding; qulconeogenesis; homotetramer; ligase; zinc C;Reywords: biotin carboxylase homology eACHS-F;157-331/Domain: biotin carboxylase homology eACHS-F;157-331/Domain: ATP/bloarbonate binding #status predicted <ATB1>F;557-468/Domain: ATP/bloarbonate binding #status predicted <ATB2>F;569-908/Domain: ATP/bloarbonate binding #status predicted <ATB2>F;1056-1169/Domain: lipoyl/biotin-binding homology <LPB>F;1135/Binding site: biotin (Lys) (covalent) #status experimental
Pyruvate carboxylase (EC 6.4.1.1) 1 [validated] - yeast (Saccharomyces cerevisiae) N;Alternate names: protein G3428; protein XGL062w; pyruvic carboxylase C;Species: Saccharomyces cerevisiae C;Date: 31-Dec-1991 #sequence_revision 19-Jul-1996 #text_change 01-Feb-2002 C;Accession: S64066; A29233; S05760; A29722 R;Feuermann, M.; Potier, S.; Souciet, J.L. Submitted to the Protein Sequence Database, May 1996 A;Reference number: S64044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 TAAKKAGLPVLAEST-PSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 FQRATSEARTAFGNGTCFVERFLDKPKHIEVQLLADNHGNVVHLFERDCSVQRRHQKVVE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 KILVANRGEIPIRIFRTAHELSMOTVAIYSHEDRLSTHKOKADEAYVIGEVGOYTPVGAY
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Blochem Biophys. Res. Commun. 145, 390-396, 1987
A; Title: Veast pyruvate carboxylase: gene isolation.
A; Reference number: S05760; MUID:87241529; PMID:3036126
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A;Cross-references: SGD:S0003030; MIPS:YGL062w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1003-1178 <MOR>
A; Cross-references: EMBL:J03889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1124-1149 <MOR2>
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380	429 440	485	500	535	58	595	618	655	678	715	736	774	962	834	55	894	915	954	972	1002	1030	1061	680	120	1149		
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321	371	430	441	486	501	536	559	296	619	929	619	716	737	775	797	835	856	895	916	955	973	1003	1031	1062	1090	1121	1150
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Search completed: September 24, 2003, 16:00:32 Job time: 39.741 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 24, 2003, 15:44:03; Search time 18.3631 Seconds (without alignments) 2919.469 Million cell updates/sec Run on:

US-09-974-973A-19 5788 1 MSTHTSSILPAFKKILVANR......RVVVPAATKVEGGDLIVVVS 1140 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		005920 musculu					P78992 pichia past	Q58626 methanococc	Q06862 anabaena sp	archaeogl		P43873 haemophilus		Q8x9b6 escherichia	P37798 pseudomonas		_	P46401 mycobacteri		P46392 mycobacteri	Q58628 methanococc		-	-		P32528 saccharomyc					_		bos t	Q28559 ovis aries
SUMMARIES	a	PYC_MOUSE	PYC_RAT	PYC_HUMAN	PYC1_YEAST	PYC2_YEAST	PYC_PICPA	PYCA_METJA	ACCC_ANASP	PYCA_ARCFU	PYCA_METTH	ACCC_HAEIN	ACCC_ECOLI	ACCC_ECO57	ACCC_PSEAE	MCCA_HUMAN	MCCA_MOUSE	BCCA_MYCTU	ACCC_BACSU	BCCA_MYCLE	PYCB_METJA	PCCA_HUMAN	MCCA_SOYBN	MCCA_ARATH	PCCA_RAT	DUR1_YEAST	PYCB_METTH	DCOA_SALTY	DCOA_KLEPN	COA1_RAT	COAC_CHICK	COA1_HUMAN	COA1_BOVIN	COA1_SHEEP
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эÞР	Query	4	43.6	43.5	$^{\circ}$	2	н	18.6	7	7	7	9	9	9	9	S	S	15.3	rU.	Ω.	2	S)	4	₹.	4	14.4	4		ω,	0	0	10.5		10.4
	Score	541.	2525.5	27	2457	2436	2391	1079	1036.5	1019	266	946	938	936	924	911		883.5	879	875.5	871.5	1	859.5	859	843.5	835.5	825	804	799.5	612.5	609.5	609.5	608.5	109
	Result No.	1	n	m	4	5	91	7	ж Э	on (10	11	12	13	1.4	15	91	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	35	λ. λ.

homo sapien	saccharomyc	saccharomyc	schizosacch	archaeoglob	methanobact	escherichia	escherichia	vibrio vuln	thermotoga	salmonelía	Q87sf3 vibrio para
000763	P32874	000955	P78820	028994	027077	Q8xa38	P00968	Q8dem2	Q9wz27	P14846	Q87sf3
COA2 HUMAN	HFA1_YEAST	COAC_YEAST	COAC_SCHPO	CARB_ARCFU	CARB_METTH	CARB_ECO57	CARB_ECOLI	CARB_VIBVU	CARB_THEMA	CARB_SALTY	CARB_VIBPA
, 	Н	Н	Н	Н	H	Н	Н	Н	Н	Н	Н
2483	2273	2233	2280	1076	1060	1072	1072	1077	1099	1074	1077
7.6	9.6	6.9	8.8	4.6	4.6	4.4	4.4	4.4	4.4	4.3	4.3
	υ.	37.5	511	267.5	264	255	255	254.5	253.5	251.5	251.5
561.5	556	Ś									

ALIGNMENTS

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669 TAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLV 728
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Last annotation update)
mitochondrial precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last seq 28-FEB-2003 (Rel. 41, Last SPB-2003 (Rel. 41, Last Paruvate carboxylase, mitochon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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SEQUENCE FROM N.A.
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P52873; Q64555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  638 PFQMLLRGANAVGYTNYPDNVVFKFCEVAKENGMDVFRVFDSLNYLDNMLLGMBAGSAG 697
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                                                                                                                                                                                                                                                                                                                                                                                                                               38 KKVMVANRGEIAIRVFRACTELGIRTVAVYSEQDTGQMHRQKADEAYLIGRGLAPVQAYL 97
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                                                                                                                                                                    Manganese; Gluconeogenesis;
                                                                                                                                                                                                                      BIOTIN CARBOXYLASE (BY SIMILARITY). CARBOXYLTRANSFERASE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1178;
                                                                                                                                                                                                                                                  BIOTIN CARBOXYL CARRIER PROTEIN (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                               Lipid synthesis; Transit peptide MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                Query Match
43.9%; Score 2541.5; DB 1; Length
Best Local Similarity 47.0%; Pred. No. 6.7e-129;
Matches 537; Conservative 187; Mismatches 401; Indels
                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BIOTIN (BY SIMILARITY).
W; 14CEA0F9DA8B8127 CRC64;
                                                                                                                                                                                                           PYRUVATE CARBOXYLASE
                                                                                                                                     TIGRFAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
Ligase; Multifunctional enzyme; Biotin;
                                                 Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00864; biotin_lipoyl; 1.
Pfam; PF00289; CPSase_L_Chain; 1.
Pfam; PF00786; CPSase_L_D2; 1.
Pfam; PF00682; HMCL-like; 1.
Pfam; PF02436; PYC_OADA; 1.
                                        IPR005930; Pyruv_carbox.
 IPR005481; CPase_L_N. IPR000891; HMGL-like. IPR003379; PYC_OADA.
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                                                                                                                                           845
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                                              729 TALRREF-DLPVHYHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSAIVAA
                                                                         877 QAHSMGLGSKFKEVKKAYVEANQMLGDLIKVTPSSKIVGDLAQFMVQNGLSRAEAEAQAE
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                                                                                                                                           FAHTREDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGR--VYRHEIPGGQLSNLRA
                                                                                                                                                                      817 TKGTPLDTEVPLERVFDYSEYWEGARGLYAARDCTATMKSGNSDVYENEIPGGQYTNLHF
                                                                                                                                                                                                                                   QATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQ
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BLOCHEM. J. 316:631-637(1996).

-!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY) AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.

-!- CATALYTIC ACTIVITY: ATP + PYRUVATE + HCO(3)(-) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 6.4.1.1) (Pyruvic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.A., Moran S.M., Macdonald M.J.; sequence of the rat pyruvate carboxylase-encoding cDNA."; 165:331-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Wistar; TISSUE=Liver;
MEDLINE=96257760; PubMed=8687410;
Jitrapakdee S., Booker G.W., Cassady A.I., Wallace J.C.;
"Cloning, sequencing and expression of rat liver pyruvate
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466

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DRSVESVTATAEKADSSNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATIT 1112
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                                                                                                                                                                                                                     LQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQL-GGEITAHFDSMLVKMTCRG 406
                                                                                                                                                                                                                                                         434 KDHPTAATKMSRALAEFRVRGVKTNIPPLQNVINNQQFLAGIVDTQFIDENPELFQLRPA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 ARDLREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYD 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             733 AGTHILCIKDMAGLLKPAACTMLVSSLRDRFPDLPLHIHTHDTSGSGVAAMLACAQAGAD 792
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VDEKGNHVF.IEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAA
                                                                                                                            467 DDEQGRILDYLADVTVNKPHGVRPKDVA-APIDKL-PNIKDLPLPRGSRDRLKQLGPAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 QNRAQKLLHYLGHVMVNGPTTPIPVKVSPSPVDPIVPVVPIGPPPAGFRDILLREGPEGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48
                                                                                                                                                   LIPOAMIDE TRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 AGVRFIGPSPEVVRKMGDKVEARAIAIAAGVPVVPGTNSPINSLHEAHEFSNTYGFPIIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOTIN CARBOXYL CARRIER PROTEIN
(BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY).
BOTIN (BY SIMILARITY).
D -> S (IN REF. 2).
C -> I (IN REF. 2).
G -> R (IN REF. 2).
G -> R (IN REF. 2).
WW; 8E5FA19BC132A8DD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410; Indels
             COFACTOR: BIOTIN AND MANGANESE (BY SIMILARITY).
PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
SUBUNIT: HOMOCETARMER (BY SIMILARITY).
SUBCELLULAR LOCATION: MITOCHONDRIAL MALLIX,
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES,
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2525.5; DB 1
Pred. No. 4.8e-128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001882; Biotin_attach.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005493; Biotin_lipoyl.
InterPro; IPR005479; CPase_L_D2.
InterPro; IPR005481; CPase_L_N.
InterPro; IPR005491; CPase_L_N.
InterPro; IPR00391; PYC_OADA.
InterPro; IPR005991; PYC_OADA.
Fam; PF02785; Biotin_carb_C; IPR06599; PYTUV_carbox.
Pfam; PF00364; biotin_lipoyl; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR01235; PYruv_carbox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00289; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129689 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF02786; CPSase_L_D2; 1. PF00682; HMGL-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U36585; AAC52668.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S68252; JC4391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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ACT_SITE
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CONFLICT
SEQUENCE
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J. Hum. Genet. 62:1312-1319(1998).

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A MEDLINE-2238625; Pubbmed-12477932;

A Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alasner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Brownstein M.J., Usdin T.B., Tonaldom M.F., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.W., Krzywinski M.I., Skalsku U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RY Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1083-1178 FROM N.A.
SEQUENCE OF 1083-1178 FROM N.A.
MEDLINE-87212051; Pubmed-3555348;
Lamhonwah A. M., Quan F., Gravel R.A.;
Lamhonwah A. M., Quan F., Gravel R.A.;
"Sequence homology around the biotin-binding site of human propionyl"
"Sequence homology around the carboxylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS PC DEFICIENCY THR-610 AND ILE-743.
MEDLINE-98954451; PubMed-9585612;
Carbone M.A., Mackay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,
Felgenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,
Seargeant L., Robinson B.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85030380; PubMed-6588474; Freytag S.O., Collier K.J.; Molecular cloning of a cDNA for human pyruvate carboxylase. Structural relationship to other biotin-containing carboxylases and regulation of mRNA content in differentiating preadipocytes."; J. Biol. Chem. 259:12831-12837(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amerindian pyruvate carboxylase deficiency is associated with two distinct missense mutations.";
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                          Wexler I.D., Du Y., Lisgaris M.V., Mandal S.K., Freytag S.O., Yang B.-S., Liu T.-C., Kwon M., Patel M.S., Kerr D.S., "Primary amino acid sequence and structure of human pyruvate
                                                                                                                                                                                                                                                                                                                                                                                       Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H., "cDNA cloning of human kidney pyruvate carboxylase."; Biochem. Biophys. Res. Commun. 202:1009-1014(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-Kidney, and Liver; Walker M.E., Jitrapakdee S., Val D.L., Wallace J.C.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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TISSUE-Kidney, and Liver;
MEDLINE-95002202; PubMed=7918683;
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94324922; PubMed=8048912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1135-1178 FROM N.A.
                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney
                                                                                                                                                                                                                                                                 carboxylase.
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                                                                                                                                                      Pediatr. Res. 43:579-584(1998).

-i-FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTHN IN THE FIRST STEP AND THE TRANSFER OF THE
CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)
AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIE FROM PYRUVATE.

-i- CATALYTIC ACTIVITY: ATP + PYTUVATE + HCO(3)(-) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                     MEDLINE~98244401; PubMed-9585002;
Wexler I.D., Kerr D.S., Du Y., Kaung M.M., Stephenson W., Lusk M.M.,
Wappner R.S., Higgins J.J.;
"Molecular characterization of pyruvate carboxylase deficiency in two
consanguineous families.";
                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Mitochondrial matrix.

SUBCELLULAR LOCATION: Mitochondrial matrix.

DISFASS: Defects in PC are the cause of pyruvate carboxylase deficiency (PC deficiency) [MIM:266150] leading to lactic acidosis, mental retardation and death. It occurs in three forms: mild or type A, severe neonatal or type B, and a very mild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis; ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRUVATE CARBOXYLASE.
BIOTIN CARBOXYLASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM) 266150; -. GO: 0005524; F:ATP binding activity; TAS. GO: 0009374; F:blotin binding activity: TAS. GO: GO:0004736; F:private carboxylase activity: TAS.
                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS. SUBUNIT: Homotetramer.
                                    VARIANTS PC DEFICIENCY ALA-145 AND CYS-451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR005849; Biotin_lipoyl.
InterPro; IPR005499; CPase_L_D?
InterPro; IPR005499; CPase_L_N?
InterPro; IPR005499; PYC_OADA.
InterPro; IPR005379; PYC_OADA.
InterPro; IPR005379; PYC_OADA.
InterPro; IPR00530; PYTUV_CATDA.
InterPro; IPR005399; PYC_OADA.
InterPro; IPR00539; PYC_OADA.
InterPro; IPR00589; CPase_L_C; I.
IPFam; PF00789; PYC_CADA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR01235; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                               COFACTOR: BIOTIN AND MANGANESE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 572370; AAB31500.1; -.
EMBL; 672370; AAB31500.1; -.
EMBL; 030891; AAA82937.1; -.
EMBL; BC011617; AAH11617.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M26122; AAA36423.1; -.
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HSSP; P24182; IBNC.
Genew; HGNC:8636; PC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lacticacidemia.
                                                                                                                                                                                                                                                                                                                              oxaloacetate.
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GK; P11498; -
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Db 679 SLNYLPNMLLGMEAAGSAG-GVVEAAISYTGDVADPSRTKYSLQYYMGLAEELVRAGTHI 737 Qy 710 IAIKDMAGLLRPAAVTKIVTALRREF-DLPVHVHTHDTAGGQLATYFAAQAGADAVDGA 768	QY 887 ALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGR 940 Db 1: : :	OY 1060 VTATAERADSSNKGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGK 1118 1097 EMHFHPRALKDVKGGIGAPMPGKVIDIKVVAGAKVAKGQPLCVLSAMKMETVVTSPMEGT 1156 OY 1119 IDRVVVPAATKVEGGDLIVVV 1139 1157 VRKVHVTKDMTLEGDDLILEI 1177	RESULT 4 PYC1_YEAST ID PYC1_YEAST AC P11154; DT 01-0TU-1989 (Rel. 11, Created) DT 01-0CT-1996 (Rel. 34, Last sequence update) DT 28-PEB-2003 (Rel. 41, Last annotation update) DE PYLVATE carboxylase 1 (EC 6.4.1.1) (Pyruvic carboxylase 1). GN PYC1 OR PYV OR YGL062M. OS Saccharomyces cerevisiae (Baker's yeast). OS Bustryota; Fungi, Ascomycota, Saccharomyceties; OC Eukaryota; Fungi, Ascomycota, Saccharomycetes; OC Saccharomycetales; Saccharomycetes.	OX NCBL_TaxID=4932; RN [1] RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. RX MEDLINE=88298805; PubMed=3042770; RA Lim F., Morris C.P., Occhiodoro F., Wallace J.C.; RT "Sequence and domain structure of yeast pyruvate carboxylase."; RL J. Biol. Chem. 263:11493-11497(1988). RN [2] RN SEQUENCE FROM N.A. RC STRAIN=52880. RX MEDLINE-97377993; PubMed=9234674;	RA Feuermann M., de'Montigny J., Potier S., Souciet JL.; RT "The characterization of two new clusters of duplicated genes RT "The characterization of two new clusters of duplicated genes RT chromosomes."; RL Yeast 13:861-869(1997). RN [3] RP SEQUENCE OF 1003-1178 FROM N.A. RS MONTINE-87241529; PubMed-3036126; RA MONTIS C.P., Lim F., Wallace J.C.; RT "Yeast pyruvate carboxylase: gene isolation."; RT "Yeast pyruvate Carboxylase: gene isolation."; RL Biochem. Biophys. Res. Commun. 145:390-396(1987). CC INVOLVING THE ATP-DEPENDENT CARBOXYLASE CAPAIYZES A 2-STEP REACTION, CC TINVOLVING THE ATP-DEPENDENT CARBOXYLASION OF THE COVALENTLY CC CARBOXYL GROUP TO PYRUVATE IN THE SECOND.
	CONFLICT 225 226	QY 6 SSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRS 53 1	114 IGPTPEVLDLTGDKSRAVTAAKKAGLPVL-AESTPSKNIDEIVKSAEGGTYPIEVKAVAG [: : : : : : : : : : : : :	OY 293 NHVFTEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRI 352 DD 11 1 1 1 1 1 1 1 1	

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                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 TAAKKAGLPVLAEST-PSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 KILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEG--SPVKAY 71
                                                                                                  SUBCELLULAR LOCATION: CYLOPLASMIC, SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS: TIGRO135; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN: 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Gaps
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V -> D (IN RE-
R -> A (IN RE-
C -> C (IN REF. 1).
A -> R (IN REF. 1).
E -> Q (IN REF. 1).
C -> K (IN REF. 1).

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60; 60:0004736; F:pyruvate carboxylase activity; IDA.
InterPro; IPR001882; Biotin_attach.
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OTIN (BY SIMILARITY).
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BIOTIN (BY
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InterPro; IPR000698; Biotin_lipoyl.
InterPro; IPR000698; Biotin_lipoyl.
InterPro; IPR000691; Biotin_lipoyl.
InterPro; IPR000691; BMGL-like.
InterPro; IPR000891; BMGL-like.
InterPro; IPR000891; PVC_ADA.
InterPro; IPR005930; PVL_CADA.
InterPro; IPR005930; PVL_CADA.
INTERPRO; IPR005930; PVL_CADA.
IPFam; PF002785; Biotin_carb_c; IPFam; PF002785; Biotin_lipoyl; IPFam; PF00289; CFSase_L_Chain; I.
IPFam; PF00289; CFSase_L_Chain; I.
IPFam; PF002785; GFSase_L_D2; I.
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                                            COFACTOR: BIOTIN AND ZINC.
                                                              PATHWAY: Gluconeogenesis.
                                                                                                                                                                                                                                                                                                                                                           EMBL; J03889; AAA34843.1; -.
EMBL; Z72584; CAA96765.1; -.
PIR; S64066; QYBYP.
                                      -!- COFACTOR: BIOTIN AND Z:
-!- PATHWAY: Gluconeogenes:
-!- SUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: (
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462
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909 90
1178 AA;
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S0003030; PYC1
                      oxaloacetate.
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                           IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 310
                                                                                                                                                                                      EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 370
                                                                                                                                                                                                                                                                               YRSPGGAGVRLDGA-AQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 QIGLPKLKSNP--SVPHLHDAQGNVINVTKSAPPSGWRQVLLEKGPAEFARQVRQFNGTL 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              596 DRIDBELREAMPNVNIQMELRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVS 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     716 AGLIRPAAVTKIVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPISG 774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       895 VDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEE 954
191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHIGEVVHLYERDCSLQRRHQKVVE
                                                                                                                      430 INIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVN----KP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486 HGVRPKDVAAPIDKLPNIKDL------PLPRGSRDRLKQLGPAAFARDLREQDALA
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P32327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- INDUCTION: By glucose.
-!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHAIE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PYRUVATE CATDOXYlase 2 (E. 6.4.1.1) (Pyruvic carboxylase 2) (PCB 2).
PYC2 OR YBR218C OR YBR1507.
                                                                                                                                                                                                                                                                                                               Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A. Scherens B., Vierendeels F.;
                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                     Stucka R., Dequin S., Salmon J.-M., Gancedo C.;
"DNA sequences in chromosomes II and VII code for pyruvate
carboxylase isoenzymes in Saccharomyces cerevisiae: analysis of
pyruvate carboxylase-deficient strains.";
Mol. Gen. Genet. 229:307-315(1991).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-96128067; PubMed-8554526;
Val D.L., Chapman-Smith A., Walker M.E., Cronan J.E. Jr.
Wallace J.C.,
                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyruvate carboxylase activity; IDA,
                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                      SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-92017667; PubMed=1921979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Homotetramer, SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UnterPro; IPR001882; Biotin_attach.
InterPro; IPR005482; Biotin_attach.
InterPro; IPR005482; Biotin_axb_C.
InterPro; IPR005479; Clase_L_D2.
InterPro; IPR005481; CPase_L_D2.
InterPro; IPR005481; CPase_L_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR005930; Pyruv_carbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPSase_L_chain; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biotin_carb_C; 1.
biotin_lipoyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: BIOTIN AND ZINC. PATHWAY: Gluconeogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005829; C:cytosol; IDA
GO; GO:0004736; F:pyruvate carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003379; PYC_OADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X59890; CAA42544.1; -.
EMBL; Z36087; CAA85182.1; -.
EMBL; U35647; AAC49147.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S46094; S46094.
HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S0000422; PYC2
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oxaloacetate
                                                                                                                            NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00364;
                                                                                                                                                                                                                                                                                                  STRAIN=S288c;
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CPSase_L_D2; 1.

PF02786;

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16;
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                                                                                                                                                                                                                                                                                                                                                                                -SPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLT 124
                                                                                                                                                                                                                                                                                                                                                                                             184 PDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDKVSARHLAARANVPTVPGTPGPIETVQEALDFVNEYGYPVIIKAAFGGGGRGMRVVRE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 RHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIGIITAYRSPGGAGVRLDGA-AQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 FTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTV 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 STLPAFKKILVANRGETAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEG- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRIRGVKTNIPFLLTLLTNPVFIEGTYWTTFIDDTPQLFQMVSSQNRAQKLLHYLADLAV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGSSIKGQIGLPKLKSNP--SVPHLHDAQGNVINVTKSAPPSGWRQVLLEKGPSEFAKQV 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIF 648
                   TIGREAMS; TIGRO1335; pyruv_carbox; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                        15 SILGEKNKILVANRGEIPIRIFRSAHELSMRTIAIYSHEDRLSMHRLKADEAYVIGEEGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N----KPHGVRPKDVAAPIDKLPNIKDL------PLPRGSRDRLKQLGPAAFARDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 REQDALAVIDITFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMR
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                            Length 1180;
                                                                                                                                                                                                                                                                                                                   408; Indels
                                                                                                                                                                                                                                                                       AD60DA3A60F5E001 CRC64;
                                                                                                                                                                                          (IN REF. 1).
REF. 1).
                                                                                                                                                                                                                                                            -> KVIFTR (IN REF.
                                                                                                                                                                                                                                                                                            42.1%; Score 2436; DB 1;
45.5%; Pred. No. 3.1e-123;
                                                                                                                                                          (IN REF.
(IN REF.
STR (IN R
                                                                                         ATP (POTENTIAL)
                                                                                                                                                                                                                                     (IN REF.
                                                                                                                                                                                                                REF.
                                                                                                                                                                                                                                                                                                      al Similarity 45.5%; Pred. No. 3.1e 531; Conservative 183; Mismatches
                                                                                                    BY SIMILARITY
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                                                                                                                BIOTIN
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PF00682; HMGL-like; 1. PF02436; PXC_OADA; 1.
                                                                      Zinc; Multigene family.
NP_BIND 183 188
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268
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546
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773
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                                                                                                   ACT_SITE
BINDING
                                                                                                                                             CONFLICT
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996 DDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDK-GMRNVVANVNGQIRPMRVRD 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCRPGLELEPFDLE--KIREDLQNRFGDIDECDVASYNMYPRVYEDFQKIRETYGDLSVL 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                  DALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAH 708
                                                                                                                        709 ILAIKDMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDG 767
                                                                                                                                                                                                                                                                                                LHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPL 947
                                                                                                                                                                                                                                                          ASAPLSGITSQPSLSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGIPGPT 827
                                                                                                                                                                                                                                                                                                                                                                                      GRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: BIOTIN AND ZINC.
PATHWAY: Gluconeogenesis.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: WITH OTHER BIOTIN CARBOXXLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                948 TEVPEEEQAHLDADDSKERRNSLNRL------LFPKPTEEFLEHRRRFGNTSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        910 QFWYSNKLTSDDIRRLANSLDFPDSVMDFFEGLIGQPYGGFPEPLRSDVLRNK---RRKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
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Menendez J., Delgado J., Gancedo C.;
"Isolation of the Pichia pastoris PYC1 gene encoding pyrun carboxylase and identification of a suppressor of the pyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pichia pastoris (Yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1189 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1144 PADGQVKDVFIKDGESVDASDLLVVL 1169
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Yeast 14:647-654(1998)
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P78992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 QYSPVQAYLAIDEIIKIAVKHNVNMIHPGYGFCSENSEFARKVEENGILWVGPSDTVIDA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 TGDKSRAVTAAKKAGLPVLAEST-PSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 VGDKVSARNLAYAANVPTVPGTPGPIEDVAQATAFVEEYGYPVIIKAAFGGGGRGMRVVR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDTGIITAYRSPGGAGVRLDGAAQLGGE-ITAHFDSMLVKMTCRGSDFETAVARAQRALA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || : || || || || || || || 436 EFRIRGVKINIPFLLALLTHPVFMTSECWTTFIDDTPELFKILTSQNRAQKILAYLGDLA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KPHGVRPKDVAAPIDKLPNIKD--LPLPRGSRDRLKQLGPAAFARDL 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 SPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.3%; Score 2391; DB 1; Length 1189; 45.3%; Pred. No. 8.2e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1140 1140 BIOTIN (BY SIMILARITY).
1189 AA; 131400 MW; 8B6E858079657914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                        InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_carb_C.
InterPro; IPR005483; Biotin_lipoyl.
InterPro; IPR005483; CPase_L.
InterPro; IPR005483; CPase_L.D2.
InterPro; IPR005481; CPase_L.D2.
InterPro; IPR001891; PRC_CABA.
InterPro; IPR001891; PRC_CABA.
InterPro; IPR001891; PYCU_CABA.
InterPro; IPR005930; PYCU_CABA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO1235; Pyruv_carbox; 1. PROSITE; PSO0188; BIOTIN; 1. PROSITE; PSO0866; CPSASE_1; 1. PROSITE; PSO0867; CPSASE_2; 1.
                                                                                                           EMBL; Y11106; CAA71993.1; -. HSSP; P24182; 1DV1.
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02436; PYC_OADA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00098; CPSASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190
315
1140
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es 526; Conserv
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NP_BIND
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945 APLTEVPEEEQA---HLDADDSKERRNSL-NRLLFPKPTEEFLEHRRRFGNTSALDDREF 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1001 FY--GLVEGRETLIRLPDVRTPLLVRLDAISE-PDDKGMRNVVANVNGQIRPMRVRDRSV 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1031 LSPPKIDEERHYTIVTIETRKTLIIKCMAEGELSQSSGTREVYFELNGEMRKVTVEDKNG 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1058 ESVTATAEKADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVD 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNGSSIKGQIGLPKLH--KEADIPSIIDINGDVIDVSIPPPDGWRQFLLEKGPEQFAQQV 553
                                                               649 DALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAH 708
                                                                                                                                                                                                                                                                          709 ILAIKDMAGLLRPAAVTKLVTALRREF-DLPVHVHTHDTAGGQLATYFAAAQAGADAVDG 767
                                                                                                                                                                                                                                                                                                 888 LHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSE---GK 944
                                                                                                                                                                                                                                 DALNDIEGLKVGVDAVKKAG-GVVEAIMCYSGDMLKPGKK-YNLEYINLAIELVEMGTH
                                         REQDALAVIDITFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMR
                                                                                                                  FLFEDPWDRLDELREAMPNVNIQMLLRGRNIVGYTPYPDSVCRAFVKEAASSGVDIFRIF
                                                                                                                                               614 FLHEDPWQRLRKLRKAVPNIPFSMLLRGGNGVAYYSLPDNAIDHFLKQAKDTGVDVFRVF
                                                                                                                                                                                                                                                                                                                                                    768 ASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPT
                                                                                                                                                                                                                                                                                                                                                                                         RVNSMSGMTSQPSMSAFIASL-DGEIETGIPEANAREIDAYWAEMRLLYSCFEADLKGPD
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MEDLINE-96337999; PubMed-8688087;
BRILT C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
Complete genome sequence of the methanogenic archaecon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYCA OR M11229.
Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcaceae;
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Q58626;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 TAAKKAGLPVLAESTPS-KNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
                                                                                                                                  Arch. Microbiol. 174:406-414(2000).
-!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
GROUP TO PYRUVATE IN THE SECOND.
                                                                                                                                                                                                                                                                                                                                                                                                        IS 80-90 DEGREES CELSIUS.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
                                                                                                                                                                                                                                                                                         BY MAGNESIUM, WHEN ITS CONCENTRATION HIGH CONCENTRATION OF ATP AND ALPHA-
                                                                                                                                                                                                                      CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate oxaloacetate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00866; CPSASE 1, 1.
PROSITE; PS00867; CPSASE 2; 1.
Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FNKVLIANRGEIAIRIIRACWELGIKTVAVYSEADKRSLHATLADEAYCIG-PAFAAKSY
                                                                                                                                                                                                                                                                                                                                     PATHWAY: Gluconeogenesis.
SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS.
MASS SPECTROMETRY: MW-55500; METHOD-MALDI.
MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 FKKILJVANRGELAVRAFRAALETGAATVALYPREDRGSFHRSFASEAVRIGTEGSPVKAY
                                                                                                                                                                                                                                                        COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
                                                                                                    "A stable archaeal pyruvate carboxylase from the hyperthermophile Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146; Indels
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04D2E401892F872F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 7e-5;
; Mismatches
                                                                                 Mukhopadhyay B., Patel V.J., Wolfe R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.6%; Score 1079; 48.2%; Pred. No. 7e
                                                                                                                                                                                                                                                                                                                                                                                                                                            AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005483; CPase_L.
InterPro; IPR005493; CPase_L.D2.
InterPro; IPR005491; CPase_L.N.
Pfam; PF00289; CPSase_L.N.
Pfam; PF00289; CPSase_L.Chain; I.
Pfam; PF00289; CPSase_L.Chain; I.
                                                                  PubMed=11195096;
                                                                                                                                                                                                                                                                                  ENZYME REGULATION: INHIBITED EXCEEDED THE ATP ONE, AND BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Complete_proteome
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TIGREAMS; TIGR00514; accC; 1.
jannaschii.";
Science 273:1058-1073(1996).
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PIR; D64453; b64453.
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InterPro; IPR004549; Acc
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                                             SEQUENCE OF 1-12,
MEDLINE=21034791;
                                                                                                                                                                                                                                                                                                                       KETOGLUTARATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                        BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218;
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SEQUENCE
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RA MEDIATION STATES, TURNORULALING TO, KUTILZ T., Sasamoto S.,
RA MEDIATION S., MOIN C.P., KUTILZ T., Sasamoto S.,
RA MATANDE A., ITIGUCHI M., ISHIRAWA A., KAWASHIMA K., KIMUTA T.,
KAIDAMA Y., KODATA M., MATSUMNOLO M., MATSUMO A., MUTAKI A.,
RA MARZARI N., SDIMDO S., SUGIMOTO M., TARAZAWA M., YAMAGA M.,
RA YASUGA M., TADATA S.;
RY TOMORIO S., SUGIMOTO M., TARAZAWA M., YAMAGA M.,
RT TOMORIO S.,
RY TOMORIO S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
191 ATEASREAFRAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250
                                                                                                                       310
                                                                                                                                                                                                                  EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 370
                                                                                                                                                                                                                                                    YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 430
                                                                                                                                                                                                                                                                                                                                                           241 EAPSPIMTEELRERMGEAAIKAGKAINYDSAGTVEFLY-ENGNFYFLEMNTRIQVEHTVT
                                                                                                         251 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gornicki P., Scappino L.A., Haselkorn R., Rens for two subunits of acetyl coenzyme A carboxylase of Anabaena sp. strain PCC 7120: biotin carboxylase and biotin carboxyl carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-Coacarboxylase) (EC 6.4.1.2) (ACC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NIGFLRALLREEDFTSKRIATGFIADHPHLLQ 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 175:5268-5272(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=93352435; PubMed-8102363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=103690;
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132 TAAKKAGLPVLAESTPSKNID-EIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 ATEASREAERAFGDGAVYVERAVINPQHIEVQILGDHIGEVVHLYERDCSLQRRHQKVVE 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT
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16-OCT-2001 (Rel. 40, Last annotation update)
Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
PYCA OR AF0220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
8A541B38B39E00F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGRO0514; accc; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
Fatty acid biosynthesis; Ligase; Biotin; AIP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      le-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.9%; Score 1036.5; 48.4%; Pred. No. 1.1e
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send an email to license@isb-sib.ch).
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PIR, A453311, A53311.
PIR, A41923; A41923.
HSSP, P24182; 1BNC.
InterPro; IPR004549; AccC.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005481; CPase_L_D2.
InterPro; IPR05891; CPase_L_D2.
Pfam; PF02785; Biotin_carb_C; IPFam; PF02785; Biotin_carb_C; IPFam; PF02785; CPase_L_chain; IPFam; PF02786; CPase_L_chain; IPFam; PF02786; CPase_L_D2; IPFAM; PF0278
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                                                         EMBL; L14862; AAB51770.1;
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030019;
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ACT_SITE
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ID PYCA_AR
AC 3030019
DT 30-MAY-
DT 30-MAY-
DT 16-OCT-
DE PYCUVAT
GN PYCA OR
OC AFCHAGE
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                                                                                         192 TEASREABAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVBI
                                                                                                                        432 IGFLRALLREEDFTSKRIATGFIAD 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Delta H;
MEDLINE=98037514; Pubmed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98148063; PubMed=9478969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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027939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131
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                                                          MEDLINE-9804933: PubMed=9389475.
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Kletchum K.A., Dodson R.A., Tomb J.-F., White O., Nelson K.E., Retchum K.A., Dodson R.J., Graham D.E., Kyrpides N.C., Ferlaschmann R.D., Quackenbush J., Iee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., Moneil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDomid L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: PYRUYATE CARBOXYLASE CATALYZES A 2-STEP REACTION, INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL GROUP TO PYRUYATE IN THE SECOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: ATP + PYTUVATE + HCO(3)(-) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FSKILVANRGEIAVRVMRACRELGIKTVGVYSSADKRAFHRVYADECYYIG-KADPRDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00866; CPSASE_1, 1.
PROSITE; PS00867; CPSASE_2; FALSE_NEG.
Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
APP-binding; Complete proteone
APP- APP- Diding; Lomplete proteone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND BICARBONATE (BY SIMILARITY).

PATHMAY: Gluconeogenesis.

SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS (BY
                                                                                                                                                                                                                                                                                                                                                                             hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39B765F319235AD1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperth reducing archaeon Archaeoglobus fulgidus."; Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                STRAIN=VC-16 / DSM 4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004549; AccC.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005491; CPase_L_D2.
InterPro; IPR005491; CPase_L_N.
Pfam; PP002785; Biotin_carb_C; IPfam; PF00289; CPSase_L_chain; IPF00289; CPSase_L_chain; IPFam; PP02786; CPSase_L_D2; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001090; AAB91012.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0514; accC; 1. PROSITE; PS00866; CPSASE 1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 47.99 hes 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D69277; D69277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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241 APSPALNEEMREELGKLAVKGAREIGYTNAGTFEFLY-ENGNFYFLEINSRLQVEHTITE 299
                                                                                                                                                              312 EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 371
                                                                                                                                                                                                                                                                                                                                                                                      RSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATN 431
252 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE
                                                                                                                                                                                                                        J. Biol. Chem. 273:5155-5166(1998).
-!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
INVOLVING THE ATP-DEPENDENT CARBOXXLATION OF THE COVALENTLY
ATTACHED BIOTHN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
GROUP TO PYRUVATE IN THE SECOND. THE MAXIMUM ACTIVITY IS AT PH 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND 60 DEGREES CELSIUS.
CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Gluconeogenesis.
SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS.
SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hong L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- ENZYME REGULATION: INHIBITED BY ADP AND ALPHA-KETOGLUTARATE.
-!- PATHWARY: GLUCOMEOGENESIS.
-!- SUBGNIT: HETEROCTAMER OF FOUR A AND FOUR B SUBGNITS.
-!- SIMILARITY: WITH OTHER BIOTIN CARBOXXLASES, LIPOAMIDE TRANSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mukhopadhyay B., Stoddard S.F., Wolfe R.S.; "Purification, regulation, and molecular and biochemical characterization of pyruvate carboxylase from Methanobacterium thermoautotrophicum strain deltaH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 AA.
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us-09-974-973a-19.rsp

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HSSP; P24182; 1BNC.
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 AA;
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                  310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 TAAKKAGLPVLAESTPS-KNIDEIVKSAEGQIYPIFVKAVAGGGGRGMRFVASPDELRKL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KIMKKAGVPVIPGIDQGVSDPDEAARIADSIGYPVIIKASAGGGGIGMRAVYEEDELIRA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 430
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                                                                                                                                                                                                                                                                                                                                                                         12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY 71
                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MESTQSVAASAFGDPTVYIEKYLERPRHIEFQVMADESGNVIHLADRECSIQRRHQKLIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT
                                                                                                                                                                                                                                                           Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
                                                                                                                                                                                                                                                                                                                                                         6; Gaps
                                                                                                                                                                                                                                                                                                                                  Length 491;
                                                                                                                                                                                                                                                                                                                                                      Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                         54656 MW; 5789C34DA7475C2E CRC64;
                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                Score 997; DB 1;
Pred. No. 1.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 TIPFHKAIMRNEAFRRGELHTHFVDEY 443
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 AND CARBAMYL PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                      PIR; A69123; A69123.
HSSP; P24182; 1BNC
InterPro; IPR004549; AccC.
InterPro; IPR005402; Biotin_carb_C.
InterPro; IPR005479; CPase_L_D2.
InterPro; IPR005481; Biotin_carb_C.
Pfam; PF02785; Biotin_carb_C; IPfam; PF02785; Biotin_carb_C; IPfam; PF02786; CPsase_L_ohain; I.
Pfam; PF02786; CPsase_L_ohain; I.
                                                                                                                                                                                                                                                                                                                                                     79;
                                                                                                                                                                                                                          TIGREAMS, TIGROD514; accc; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
                                                                                                                                                                                                                                                                       ATP-binding; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 32, Created)
(Rel. 32, Last sequ
(Rel. 41, Last anno
                                                                                                               EMBL; AE000942; AAB86377.1; -.
                                                                                                                                                                                                                                                                                                                                17.2%;
                                                                                                                                                                                                                                                                                                                                       Local Similarity 45.99
les 205; Conservative
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                                                                                                                                                                                                                                                                                                         491 AA;
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01-NOV-1995 (
28-FEB-2003 (
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ID ACCC_HAEIN
AC P43873;
DT 01-NOV-1995
DT 28-FEB-2003
                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                        MEDIATRE-95250630; PubMed=7542800;

MEDIATRE-95250630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.T., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Wenter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
                                                                                                                            Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 448;
Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA carboxylase) (EC 6.4.1.2) (ACC).
ACCC OR HI0972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2B497E2A31ED96D1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.3%; Score 946; DB 1; L. 47.6%; Pred. No. 8.3e-44; Live 61; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
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InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005479; CPase_L_D2.
InterPro; IPR005481; CPase_L_D2.
Pfam; PF02785; Biotin_carb_C; I.
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                                                                                                                  Bacteria; Proteobacteria; Gamr
Pasteurellaceae; Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995)
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                                                                                        Haemophilus influenzae.
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122 AMKKAGVPCVPGSDGPVSNDIAKNKEIAKRIGYPIIIKASGGGGGRGMRVVRSEDALEES 181
                                                                                                                                                                                                                                          308 TVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGT 367
                                                                                                                                                                                                                                                                                                         368 ITAYRSPGGAGVRLDGAAQLGGELTAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSG 427
                                                                                                                                                                                                                                                                                                                               191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE
                                                                                                                                 182 IAMTKAEAKAAFUNDMYYMEKYLENPRHYEIQYLADTHGNAVYLAERDCSMQRRHQKVVE
                                                                                                                                                                         251 IAPAQHLDPELRDRI----CADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEH
                                                                                                                                                                                                      242 EAPAPGITEEVRRDIGSRCANA---CVEIGYRGAGTFEFLY-ENGEFYFIEMNTRIQVEH
                                                                                                                                                                                                                                                                       298 PVTEMITGVDLVKEQLRIAAGL---PISFKQEDIKVKGHAMECRINAEDPKT-FLPSPGK
                                             AAKKAGLPVL--AESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL
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Li S.-J., Cronan J.E. Jr.;
"The gene encoding the bictin carboxylase subunit of Escherichia coli
acetyl-Coa carboxylase."
J. Biol. Chem. 267:855-863(1992).
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MEDLINE-92052166; PubMed=1682920;
MEDLINE-92052166; PubMed=1682920;
Tsurd D., Anai M., Sekiguchi M., Tanabe T.;
"Acetyl-CoA carboxylase from Escherichia coli: gene organization and nucleotide sequence of the biotin carboxylase subunit.";
Proc. Natl. Acad. Sci. U.S.A. 88:9730-9733(1991).
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SEQUENCE FROM N.A.
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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01-FPB-1994 (Rel. 28, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA ACCC OR FABG OR B3256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
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Enterobacteriaceae, Escherichia
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                 properties of proteins encoded
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                                                                                                                         Waldrop G.L., Rayment I., Holden H.M.; "Three-dimensional structure of the biotin carboxylase subunit of acetyl-CoA carboxylase.";
                                                                                                                                                                                                     MEDLINE=20283656; PubMed=10821865; /
Thoden J.B., Blanchard C.E., Holden H.M., Waldrop G.L.;
"Movement of the biotin carboxylase B-domain as a result of ATP
binding.";
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L -> M (IN REF. 1).
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                                     Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed proj
in the genome of Escherichia coli K-12.";
                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
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                                                                         Electrophoresis 18:1259-1313(1997).
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InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005479; CPase_L_D2.
InterPro; IPR005481; CPase_L_N.
                                                                                                                                                                  Biochemistry 33:10249-10256(1994).
            STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
                                                                                                                MEDLINE=94347758; PubMed=7915138;
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Pfam; PF00289; CPSase_L_chain; 1.
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EMBL; M80458; AAA23409.1; --
EMBL; M81189; AAA23746.1; --
EMBL; U1897; AAA28059.1; --
EMBL; AE000404; AAC76288.1; --
PIR; JS0632; JS0632.
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TIGREAMS; TIGR00514; accc; 1.
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PROSITE; PSOO867; CPSASE_2;
Fatty acid biosynthesis; Lig
Complete proteome.
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PDB; 1K69; 05-DEC-01.
EcoGene; EG10276; accC.
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PDB; 1DV1; 09-JUN-00.
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SMTRAEAKAAFSNDMYYMEKYLENPRHVEIQVLADGQGNAIYLAERDCSMQRRHQKVVEE 242
           123 MKKAGVPCVPGSDGPLGDDMDKNRAIAKRIGYPVIIKASGGGGGRGMRVVRGDAELAQSI 182
                                               TEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVEI 251
                                                                                                                          APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 311
                                                                                                                                                 RSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATN 431
                                                                                                                                                                                                                                                                                                   EVIEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 371
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CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2) = ADP + phosphate + carboxylotin-carboxyl-carrier protein.

PATHWAY: LONG-chain fatty acid biosynthesis; first step.

SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi T., Makino K., Ohdishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                      CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (By similarity). SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Bosfai G., Hackett J., Klink S., Boutin A., Shao T., Miller L., Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., "Melch R.A., Blattner F.R.,"
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA carboxylase) (EC 6.4.1.2) (ACC).
ACCC OR 24616 OR EC$4128.
Escherichia coli 0157:H7.
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MEDLINE=21074935; PubMed=11206551;
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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Mismatches 156; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  BC5716323F6233ED CRC64;
                                                                                                                                                                                                                                                                                                                             Fatty acid blosynthesis; Ligase; Biotin; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               16.2%; Score 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                         InterPro; IPR004549; Accc.
InterPro; IPR005492; Biotin_carb_C.
InterPro; IPR005479; CPASe_L_D2.
InterPro; IPR005481; CPASe_L_N.
Pfam; PF02785; Biotin_carb_C; I.
Pfam; PF00289; CPSase_L_chain; I.
                                                                                                                         EMBL; AE005553; AAG58384.1; -.
EMBL; AP002564; BAB37551.1; -.
PIR; H91144; H91144.
                                                                                                                                                                                                                                                                   Pfam, PF02786; CPSase_L_D2, 1.
TIGRFMS: TIGRO0514, accc; 1.
PROSITE: PS00866; CPSASE_1: 1.
PROSITE: PS00867; CPSASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                49337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432 IGFLRALLREEDF 444
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                                                                                                                                                                                                                                                                                                                                                                  168
                                                                                                                                                                                                                                                                                                                                                                                                449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
200; Conserv
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P37798;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-2043737; pubmed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                biotin carboxyl carrier protein and biotin carboxylase protein of Pseudomonas aeruginosa acetyl coenzyme A carboxylase.", J. Bacteriol. 175:6881-6889(1993).
                                                                                                                                 Best E.A., Knauf V.C., "Organization and nucleotide sequences of the genes encoding the
                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3B04C77785C73541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fatty acid biosynthesis; Ligase; Biotin; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 1.3e-42;
67; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004549; AccC.
InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR005481; CPase_L_D2.
InterPro; IPR005481; CPase_L_N.
Pfam: PF02785; Biotin_carb_C; I.
Pfam; PF00289; CPSase_L_chain; I.
Pfam; PF02786; CPSase_L_chain; I.
                                                                                      SEQUENCE FROM N.A.
STRAIN-AICC 15692 / PAO1;
MEDLINE-94042851; Pubmed-7693652;
                                               Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48888 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L14612; AAA16041.1; -.
EMBL; AE00489; AAG08233.1;
PIR; B49342; B49342.
HSSP; P24182; 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00866; CPSASE_1;
PROSITE; PS00867; CPSASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:959-964(2000)
               Pseudomonas aeruginosa,
                                                                                                                                                                                                                                                                                                                                                                                opportunistic pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
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SEQUENCE
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Best Local 3
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01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 30, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Biotin carboxylase (EC 6.3 4.14) (A subunit of acetyl-CoA carboxylase)

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DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 132
                                                                                     OIPAIIAAAEVTGATAIHPGYGFLAENADFAEQIERSGFTFVGPTAEVIRLMGDKVSAKD 121
                                                                                                                            133 AAKKAGLPVLAESTPSKNIDE--IVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
                                                                                                                                                                                                                                                                          251 IAPAQHLDPELRDRICADAVKFCRSIGYOGAGTVEFLVDEKĞNHVFIEMNPRIQVEHTVT 310
                                                                                                                                                                                                                                                                                                 EEVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 370
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT HIS-464.
MEDLINB-21285633; PubMed=1140147;
Obata K., Fukuda T., Morishita R., Abe S., Asakawa S., Yamaguchi S., Yoshino M., Ihara K., Murayama K., Shiqemoto K., Shimizu N., Kondo I.; "Human biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase gene (MCCA): CDNA sequence, genomic organization, localization to chromosomal band 3q27, and expression.";
122 AMKRAGVPTVPGSDGPLPEDEETALAIAREVGYPVIIKAAGGGGGRGMRVVYDESELIKS
                                                                                                                                                                                                191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE
                                                                                                                                                                                                                           YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21299419; PubMed=11406611;
Holzinger A., Roeschinger W., Lagler F., Mayerhofer P.U., Lichtner P.,
Kattenfeld T., Thuy L.P., Nyhan W.L., Koch H.G., Muntau A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roscher A.A.; "Cloning of the human MCCA and MCCB genes and mutations therein reveal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s.
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor (EC 6 4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha subunit) (3.methylcrotonyl-CoA; carboxylase 1) (MCCase alpha subunit) (3.methylcrotonyl-CoA; carbox dioxide ligase alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallardo M.E., Desviat L.R., Rodriguez J.M., Esparza-Gordillo J., Perez-Cerda C., Perez B., Rodriguez-Pombo P., Criado O., Sanz R., Morton D.H., Gibson K.M., Le T.P., Ribes A., Rodriguez de Cordoba Ugarte M., Penalya M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The molecular basis of 3-methylcrotonylglycinuria, a disorder of leucine catabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANTS MCGI ARG-325 AND SER-385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANT MCGI PHE-535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    725 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am. J. Hum. Genet. 68:334-346(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIGFLRALLREEDF 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTELHKDLVRDAAF 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Euther NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11170888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCCC1 OR MCCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCCA HUMAN
                                                                                       62
                                                    73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-Skeletel muscle;

MEDLINE-Skeletel muscle;

MEDLINE-Skeletel muscle;

MILLE ** Feligold E.A.*, Gruse L.H., Derge J.G.,

MILLE ** Religold E.A., Gruse L.H., Schamen C.M., Schuler G.D.,

MILLE ** Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MILLE ** Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MILLE ** Altschul S.F., Jedan H., Moore T., Max S.I., Wang J., Hasteh F.,

MILLE ** Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MILLE ** Marusina K., Farmer A.A., Rubin G.M., Scheetz T.E.,

MILLE ** Nordellano M.B., Poeters G.J., Abramson R.D., Mullahy S.J.,

MILLE ** MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MILLING M., Muzny D.M., Sodergren E.J., Mark S.M.,

MILLING M., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

MILLING M., Muzny A., Sodergren E.J., Myers S., Sanchez A.,

MILLING M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

MILLING M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

MILLING M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

MILLING M., Madan J., McKernan M.J., Myers R.M.,

Mutarfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Montantion and mouse cDNA sequences. "."
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human CDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3)(-) = ADP
                                                                                        SEQUENCE FROM N.A., AND VARIANTS MCGI VAL-289; SER-385; PRO-437 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate + 3-methylglutaconyl-CoA.
--- COFACTOR: Biotin.
--- PATHWAY: Leucine catabolism.
---- SUBUNIT: Probably a dodecamer composed of six biotin-containing
                                                                                                                                                      Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N., Packman S., Baumgartner E.R., Valle D., "The molecular basis of human 3-methylcrotonyl-CoA carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: Defects in MCCC1 are the cause of 3-methylcrotonylglycinuria type I (MCGI) [MIM:210200]; also designated CGA or CG2. MCGI is a recessive disease that is characterized by muscular hypotonia and atrophy, probably of
the molecular cause of 3-methylcrotonyl-CoA: carboxylase deficiency.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLUIAR LOCATION: Mitochondrial matrix.
-!- DISEASE: Defects in MCC1 are the cause of
                                              Hum. Mol. Genet. 10:1299-1306(2001).
                                                                                                                                                                                                                                              Clin. Invest. 107:495-504(2001).
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EMBL, AF310972; AAG55095.1; -.

EMBL, AB029826; BAA99407.1; -.
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BC004214; AAH04214.1;
BC004187; AAH04187.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF310339; AAG50245.1;
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EMBL; BC004187; AAH04187
Genew; HGNC:6936; MCCCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spinal origin.
                                                                                                                                    PubMed=11181649;
                                                                                                                                                                                                                          deficiency
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363 PDTGTITAYRSP-GGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALA

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64 EGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 SPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 RRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPR 302
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METHYLCROTONYL-COA CARBOXYLASE ALPHA
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/FTIG-VAR_012790.
S -> F (in MCGI; asymptomatic form).
                                                                                                                                                                                         R InterPro; IPR000482; Biotin_carb_C.
R InterPro; IPR00089; Biotin_carb_C.
R InterPro; IPR00089; Biotin_lipoyl.
R InterPro; IPR005479; CPase_L_D2.
R InterPro; IPR005481; CPase_L_D2.
R Pfam; PF00286; CPsase_L_C.
R Pfam; PF00286; CPsase_L_C.
R Pfam; PF00286; CPsase_L_C.
R Pfam; PF00286; CPsase_L_C.
R PROSITE; PS00188; BIOTIN; 1.
R PROSITE; PS00188; BIOTIN; 1.
R PROSITE; PS00667; CPsase_L_D2; 1.
R Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide; Disease mitation; Polymorphism.
I TRANSIT 1.
A 77 MITOCHONDRION (POTENTIAL).
                    MIM; 210200; -.

GO; GO:0005759; C:mitochondrial matrix; NAS.

GO; GO:0009374; F:biotin binding activity; NAS.

GO; GO:000485; F:ebiotin metabolism; Co; GO:0006768; P:biotin metabolism; NAS.

GO; GO:0006768; P:biotin metabolism; NAS.

GO; GO:0006552; P:lewoine catabolism; NAS.

InterPro; IPR001882; Biotin_attach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R -> S (in MCG1; severe form).
/FTIG4-MR_012789.
L -> P (in MCG1; severe form).
/FTIG-VAR_012788.
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/FTId=VAR_012785.
M -> R (in MCGI).
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Matches 210; Conservative 96; Mismatches 204; Indels
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F -> L (IN REF. 3 AND 4).
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GenCore version 5.1.6
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- protein search, using sw model OM protein

September 24, 2003, 15:27:07; Search time 17.8668 Seconds (without alignments) 2699.668 Million cell updates/sec Run on:

US-09-974-973A-19

5788 1 MSTHTSSTLPAFKKILVANR.....RVVVPAATKVEGGDLIVVVS 1140 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 seqs, 42310858 residues Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

Database

Issued_Patents_AA:* ٠.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-08-485-607-3	US-09-433-043B-3	US-09-198-452A-197	US-09-252-991A-27999	US-08-662-344-2	US-09-252-991A-26980	US-08-074-121-6	PCT-US94-06447-6	US-09-252-991A-26143	US-09-328-352-6725	US-09-328-352-5587	US-09-328-352-6420	US-09-252-991A-26616	US-09-134-001C-3604	US-09-433-043B-125	US-09-252-991A-19134	US-09-252-991A-19829
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ALIGNMENTS

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IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV 120
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                                                                                          APPLICANT: Lessard, Philip A.
APPLICANT: Lessard, Philip A.
APPLICANT: Willis, Laura B.
APPLICANT: Willis, Laura B.
APPLICANT: Willis, Laura B.
APPLICANT: Stephanopoulos, Gregory
TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
FILE REFERENCE: 1533.079000
CURRENT APPLICATION NUMBER: US/09/220,081
CURRENT APPLICATION NUMBER: US/09/220,081
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
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US-09-220-081-2; Sequence 2, Application US/09220081; Patent No. 6171833
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                                                                          APPLICANT: Sinskey, Anthony J.
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Best Local Similarity 100.
Matches 1140; Conservative
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Length 1140;

DB 4; ó

100.0%; Score 5788; 100.0%; Pred. No. 0;

Mismatches

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Query Match

US-09-677-575-2

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IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV

1 MSTHISSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVR

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LDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRF

VASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCS

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LQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN

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PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG

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APPLICANT: Lessard, Philip A.
APPLICANT: Lessard, Philip A.
APPLICANT: Lessard, Philip A.
APPLICANT: Stephanopoulos, Gregory
TILLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
TILLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
CURRENT APPLICATION NUMBER: 108/09/677,575
CURRENT FILING DATE: 2000-10-03
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 36
                                                       LREAMPNVNIQMLIRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA
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                                                                                                                                                                  LREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA
                                       AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADV
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FRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRAL 420
                         AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADV 480
                                                                                                                   FRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDE 600
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                                                                      TVNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTT
                                                                                                                               LREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA
                                                                                                                                                                                                           IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR
                                                                                                                                                                                                                                   661 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLR
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TYPE: PRT ORGANISM: Corynebacterium glutamicum

DD 1021 ELVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVJATAEKADSSNKGHVAAPFA		ζŏ	252 APA
	VESVIATAEKADSSNKGHVAAPFA 1080		
OY 1081 GVVTVTVAEGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIVVVS		qq	242 APA
DD 1081 GVVTVTVAEGDEVKAGDAVALIEAMKMEATTTASVDGKIDRVVVPAATKVEGGDLIVVVS		QY	312 EVT
RESULT 3 US-08-311-731A-10		Z Z	372 RSP(
<pre>Sequence 10, Application US/08311731A Patent No. 6583266</pre>		qū	361 CDP
<pre>; GENERAL INFORMATION: ; APPLICANT: SMITH, DOUGLAS</pre>		ογ	427 GVA
; APPLICANT: MAO, JEN-I ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC	SHONGHORS OIL	qa	416 GVS
	RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR DIAGNOSTICS AND THERAPEUTICS	QY	487 GVR
; NUMBER OF SEQUENCES: 411 ; CORRESPONDENCE ADDRESS:		qa	476 GSR
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE		QY	543 DAH(
CITY: BOSTON STATE: MASSACHUSETTS		qa	111 532 DAH(
COUNTRY: USA		Oy	603 EAM
COMPUTER READABLE FORM:		qa	 592 AAMI
COMPUTER: IBM PC compatible OPERATING SYSTEM: DC-DOS ANS-DOS		QY	663 AVL
SOFTWARE: Patentin Release #1.0, Version #1.25	1.25	qa	 652 AVR
SCHOOL METERS DAILS 11,731A PITTER CAME. US/08/311,731A		Qy	723 AVTE
FILING LAIE: CLASSIFICATION: 530 ATTORNY/AGENT TNFORMATION:		QΩ	 712 AAQI
NAME: GATES, EDWARD R. REGISTRATION NIMBER 31 616		ογ	783 AIV
H 6		qq	: !!! 772 SIV
TELEPHONE: 617/20-3500 TELEPHONE: 617/20-341		δλ	843 LRAC
E E		qa	 832 LRQC
			903 DPQ
AMLINO Y: 1		ପ୍ର	
MOLECULE TYPE: protein HYPOTHETICAL: YES		ò	
; ORIGINAL SOURCE: ; ORGANISM: MYCOBACTERIUM TUBERCULOSIS US-08-311-731A-10		ga qa	
60.2%; Score 3483;	; Length 1124;	ζō	1023 VRLD
Matches 698; Conservative 151; Mismatches 251;	7; 1; Indels 22; Gaps 9;	qq 	1009 IGLE
Oy 12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY	7.1	QY	1083 VIVI
Db 2 FSKVIVANRGEIAIRAFRAAYELGVGTVAVYPYEDRNSQHRLKADESYQIGGIGHPVHAX		ପ୍ର	1069 VTVG
QY 72 LDIDELIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV	NGITFIGPTPEVLDLTGDKSRAV 131	RESULT	LT 4
Db 62 LSVDEIVATARRAGADAIYPGYGFLSENPDLAAACAAAGISFVGPSAEVLELAGNKSRAI	: : : : : : AGISFVGPSAEVLELAGNKSRAI 121	US-0	US-09-134-001C-342 ; Sequence 3428, A
QY 132 TAAKKAGLPVLAESTPSKNIDEIVKSAEGOTYPIFVKAVAGGGGRGMRFVASPDELKKLA	AVAGGGGRGMREVASPDELRKLA 191	, Par	Patent No. 63803 GENERAL INFORMAT
Db 122 AAREAGLPVLMSSAPSASVDELLSVAAGMPFPLFVKAVAGGGGGGGGRGMRRVGDIAALPEAI		K E	
Qy 192 TEASREAEAAFGDGAVYVERAVINPQHIEVOILGDHTGEVVHLYERDCSLQRRHQKVVEI	VYVERAVINPQHIEVOILGDHTGEVVHLYERDCSLGRHQKVVEI 251		TITLE OF INVENT FILE REFERENCE: CHERENT ABBITCA

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ERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTPLL 1022
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                                   AQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVTE 311
                                                           TEVDLVKAOMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 371
                                                                                                                                                                                                                                                                                           RPKDVAAPIDKLPNIKDLPL----PRGSRDRLKQLGPAAFARDLREQDALAVTDTTFR 542
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DD 1069 VTVGCVGERVGAGQTIATIEAMKMEALITANVA

DD 1069 VTVGVCVGERVGAGQTIATIEAMKMEAPITAPVA

BSC-09-134-001C-3428

Sequence 3428, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NICLEIC ACID AND ANINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: PEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C

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                                                                                                                                                                                                              9 LPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPV 68
                                                                                                                                                                                                                                EHTVTEEVTEVDLVKAQMRLAAGATL---KELGLTQDKIKTHGAALQCRITTEDPNNGFR
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                                                                                                                                                                  Length 1154;
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                                                                                                                                                            42.6%; Score 2464; DB 4;
llarity 45.4%; Pred. No. 4e-186;
Conservative 197; Mismatches 400;
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                        ORGANISM: Staphylococcus epidermidis
                                                                   NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3428
                                                                                                                                                                          Similarity
                                                                                                                                   US-09-134-001C-3428
                                                                                                                                                                          Local Simi
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                                                                                             LENGTH: 1154
                                                                                                            TYPE: PRT
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                            HLDAD------DSKERRNSINRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLV 1005
                                                                                                                                                                                              1006 EGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAE 1065
                                                                                                                                                                                                                                                                                         KADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVV 1124
                                                                    897 PADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQA 956
901 EDTVINDGYKLDFPESVVSFFKGDIGQPVNGFNKKLQDVILKGQQ----PITERPGEYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...973
SEQUENCE DESCRIPTION: SEQ ID NO: 4810:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4810, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 973 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 4810:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              1125 PAATKVEGGDLIVVV 1139
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1136 ANGDAIATGDLLVEI 1150
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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US-09-107-532A-4810
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ъ Э YLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRA 130 YLDIEGIISIAKECGADAIHPGYGLLSENLNFAQRCEEKGIIFVGPKLHHLDIFGDKIKA 130 131 VIAAKKAGL-PVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRK 189 KAAAIEAGIASIPGTDGPIASIDDALEFAKQYGYPIMIKAALCGGGRGMRVAHDEKSARE 190 EIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTV 309 TEEVTEVDLVKAQMRLAAGATL-KELGLTQDK-IKTHGAALQCRITTEDPNNGFRPDIGT 367 368 ITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVS 426 427 GVATNIGFLRALLREEDFTSKRLATGFIADHPHLLQAPPADDEQGRILDYLADVTVNKPH 486 490 GIESGEKPFYEEPRMPKDLITRTDYVT------AKNVLDAKGADALVEWIKGQENL 539 MAGLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSG 774 11 AFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKA 70 WDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDV 654 SQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKD 714 775 TISQPSLSAIVAAFAHTRRDIGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHE 834 839 MPGGQYSNLQQQAKAVGLGHRWDEIKQMYHTVNLMFGDIVKVTPSSKVVGDMALFMVQND 898 835 IPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAG 894 190 LATEASREAERADGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVV GVR------PKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDAL 535 AVTDITFRDAHQSLLATRVRSFALKPAAEAVAKLIPELLSVEAWGGATYDVAMRFLFEDP Gaps Similarity 48.0%; Score 2174; DB 4; Length 973; Similarity 48.0%; Pred. No. 2.8e-163; 4; Conservative 144; Mismatches 320; Indels 2 895 VDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGR 940 454; 487 251 310 250 595 Query Match 셤 δ g δ ď ŏ g δλ g ŏ q Q_{Y} g g g qq g g a δ δ Dp Ωÿ ò $^{\circ}$ Qγ $^{\circ}$ QQ ŏ ŏ

TAAKKAGLPVLAEST-PSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 310 EEVIEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 370 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131 371 YRSPGGAGVRLDGA-AQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVA 429 380 YRSAGGNGVRLDGGNAYAGTIISPHYDSMLVKCSCSGSTYEIVRRKMIRALIEFRIRGVK 439 430 TNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADVTVNKPHGVR 489 440 TNIPFLLTLTNPVFIEGTYWGTFIDDTPQLFQMVSSQNRAQKLLHYLADVA----- 491 490 PKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTFRDAHQSLL 549 550 ATRVRSFALKPAAEAVAKLIPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVN 609 610 IQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDAVLEINT 669 APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:3380S
CURRENT APPLICATION UNBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE PATENTIN VET: 2.1
SEQ ID NO 126
LENGTH: 694 21 KILVANRGEIPIRIFRTAHELSMQTVAIYSHEDRLSTHKOKADEAYVIGEVGOYTPVGAY 14 KILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEG--SPVKAY 191 ATEASREAERAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE VAPAKTLPREVRDAILTDAVKLAKECGYRNAGTAEFLVDNQNRHYFIEINPRIQVEHTIT Gaps Synthetic Indels 476; Length 694; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide Query Match 20.6%; Score 1192; DB 4; Best Local Similarity 28.0%; Pred. No. 9.8e-86; Matches 317; Conservative 100; Mismatches 240; Sequence 126, Application US/09433043B Patent No. 6399342 ORGANISM: Artificial Sequence Sequent No. 63955**
Patent No. 63955**
GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
APTICANT: GORNICKI, PIOTR US-09-433-043B-126 72 251 311 81 132 261 492 492 QQ Op δ g ŏ δ g q g Qγ g q QΥ ă QY Ω g δ d δy a

670 AVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVT 729

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RESULT 6 US-09-433-043B-126

QQ	492 491	qq	131 AGADLFADLHLPQQDALRENGAAIQCRITTEDPENNFWPDTGTINTYRSPGGFGIRLDVG 190
QY	730 ALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPSLSAIVAAFA 789	Qy	MTCRGSDFETAVARAQRALAEFTV
qa	492 491	đ	::: :
QY	790 HTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLSNLRAQATA 849	QY	444 FISKRIATGFIADHPHLLQAPPADDEGGRILDYLADVTVNKPHGV-RPKDVAAPIDKLPN 502
qq	492 491	qu	251 FRTGEAETAFIDAHPELLGVQAKPDIASRLLWYISDVTVNGFKGVERGSQKYYPELQY 308
Qy Dp	850 IGLADRFELIEDNYAAVNEMLGRP-TKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYD 908 	O.Y D.b	503 IKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVTDTTFRDAHQSLLATRVRSFALK 559 1
οy	909 IPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADDSKERRN 968	QY	560 PAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIOMELRGRNT 619
qq	518 517	셤	369 TVAEDMGNGLPNLFSMEVWGGATFDVAYRFLNEDPWVRLKKLRAALPHTLLQMLFRGSNA 428
Qy	969 SINRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAI 1028 ::::	da Dp	620 VGYTPYDSVCRAFVKEAASSGVDIFRI 647 : : : : : 429 VGYQNYPDNVIKAFINQAANDGVDVFRI 456
Qy	1029 SEPDDK-GMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFAGV-VTVT 1086 : : :: : :	RESULT US-09-	RESULT 8 US-09-433-043B-122
Qy Db	1087 VABGDEVKAGDAVALIEBAMKMEATITASVDGKIDRVVVPAATKVEGGDLIVVV 1139 : :	; Sequ ; Pate ; GENE ; APP	Sequence 122, Application US/09433043B Patent No. 639342 GENERAL INFORMATION: APPLICANT: HASELKORN, ROBERT
RESULT 7		, APP ; TIT	LICANT: GORNICKI, PIOTR LICONT: GORNICKI, PIOTR LICONT: OFANOBACIERIAL AND PLANT ACETYL-COA CARBOXYLASE P PREPEDENCE: APOL: 32901
US-09-6: ; Sequer ; Patent	US-09-634-238-276 ; Sequence 276, Application US/09634238 ; Patent No. 6544772	COR COR	FILE REFERENCE: ARCHISSBUS CURRENT APPLICATION NUMBER: US/09/433,043B CURRENT FILING DATE: 1999-10-25 DBYOR APPLICATION NUMBER: 00/47E
GENERAL IN APPLICANT	GENERAL INFORMATION: APPLICANT: Glenn, Matthew	PRI ; PRI ; PRI	OR FILING DATE: 1995-06-07 OR PLING DATE: 1995-06-07 OR APPLICATION NUMBER: 07/956,700
; APPLICANT ; APPLICANT ; APPLICANT	CANT: Havukala, Ilkka J. CANT: Bloksberg, Leonard, N. CANT: Lubbers, Mark W.	PRI	OR FILING DATE: 1992-10-02 OR FILING DATE: 1992-10-02 MANANE OF THE
; APPLICANT ; APPLICANT	Dekker, J Christens	SEQ ;	SOTIMARE: FALEHLIN VEI. 2.1 EQID NO 122 IDNOTH: ROS
; APPLI ; APPLI		TI	TYPE: PRT ORGANISM: Artificial Sequence
; APPLIC ; APPLIC ; TITLE	erials	A C	
; FILE	OF INVENTION: them and methods for using them. REFERENCE: 11000.104301	US-09-433	information: Feptine -043B-122
CURRE CURRE NUMBE	CURRENT APPLICATION NUMBER: US/09/634,238 CURRENT FILING DATE: 2000-08-08 NUMBER OF SEQ ID NOS: 422 SOFTWARE: FastSFO for windows Varsion 4.0	Query M Best Lo Matches	Query Match 18.0%; Score 1043.5; DB 4; Length 593; Best Local Similarity 44.6%; Pred. No. 4.4e-74; Matches 229; Conservative 81; Mismatches 180; Indels 23; Gaps 5;
; SEQ ID NO ; LENGTH: ; TYPE: P		Qy	12 FKKILVANRGEIAVRAFRAALETGAATVALYPREDRGSFHRSFASEAVRIGTEGSPVKAY 71
, ORG2 US-09-63	; ORGANISM: Lactobacillus rhamnosus US-09-634-238-276		
Query Match Best Local S	Match 18.7%; Score 1083; DB 4; Length 456; ocal Similarity 51.3%; Dred No. 2 10-77.	} 6	/z DDIDELIGAARAVADALIYOTGELDENAQUARECEENGIIFIGFTEFINDIGURKAV 131 :
Matche	Conservative 66; Mismatches 1	Qy	132 TAAKKAGLPVLAESTPSKNID-EIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
oy is	VYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRIC	qq	
ପୁ (MYVEKYTASAKHVEVQVLGDEHGHLLHLFERDCSVQRRQQKVVETAPAVALPLALRNRTC	Qy.	191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHGKVVE 250
Å 98	26/ ADAVKEVRSIGYQGAGIYEFLYDEKGNHYFIENNPRIQVEHTYTEEVTEVDIVKAQMRLA 326 72 QSAVDLMASLHYENAGIYEFLYD-GEDYYFIENNPRVOVEHTITELIIGHHIII 1 1 1 1 1 1 1 1 1	q à	182 FLAAQGEAGAAFGNAGVYIEKFIERPRHIEFQILADNYGNVIHLGERDCSIQRRNQKLLE 241 251 TADAOHIDDFIRDBICADAVKFCPGIGVOGAGTVEFTADFKGNHVFTEMNDFIOVEHTVT 310
QY	VRLD-G	7 ^{QQ}	EAPSPALDSDEREKMGOAVKAAOFILYAGAGTIEFILDRSGOFYFMINITITITITITITITITITITITITITITITITITITI
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132 TAAKKAGLPVLAESTPSKNID-EIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
                                                                                                                                                                                                   191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250
                                                                                                                                                                                                                                                                                          182 FLAAQGEAGAAFGNAGVYIEKFIERPRHIEFQILADNYGNVIHLGERDCSIQRRNQKLLE 241
                                                                                                                                                                                                                                                                                                                                                   251 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 YLPPGGPGVRIDSHVYTDYQIPPYYDSLIGKLIVWGPDRATAINRMKRALRECAITGLPT 418
                                                                                    72 IDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131
                                                                                                                              62 LNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICADHHIAFIGPTPEAIRLMGDKSTAK 121
                                                                                                                                                                                                                                                                                                                                                                               242 BAPSPALDSDLREKMGQAAVKAAQFINYTGAGTIEFLLDRSGQFYFMEMNTRIQVEHPVT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                          311 EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 430
12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY 71
                         3 FDKILIANRGEIALRIRACEEMGIATIAVHSTVDRNALHVQLADEAVCIG-EPASAKSY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS FOR USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,560A FILING DATE: 14-APR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION OUMBER: US 07/956,700
FILING DATE: 02-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARCD:152/WIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 NIGFLRALLREEDFISKRIATGFIAD 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 TIGEHORIMENPOFLOGNVSTSFVOE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08422560A Patent No. 5910626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37,259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Arnold, ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wilson, Mark B. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512-474-7577
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ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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             EEVTEVDLVKAQMRLAAGAILKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 370
                                         371 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 430
                                                                                                                                     359 YLPPGGPGVRIDSHVYTDYQIPPYYDSLIGKLIVWGPDRATAINRWKRALRECAITGLPT 418
                                                                                                                                                                                                                                419 TIGFHORIMENPQFLQGNVSTSFVQE----MNKPLDFNEIRQLLFTIAQTDIAEVTLKSD 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                       431 NIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEGGRILDYLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Haselkorp, Robert

APPLICANT: Haselkorp, Piotr

TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING

TITLE OF INVENTION: ATERIECOR

NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107
FILING DATE: CONCULTENTLY HEREWITH
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                            479 -- DVTVNKPHGVRPKDVAAPIDKLPNIKDLPLP 509
                                                                                                                                                                                                                                                                                                                     475 DFELTVRKAVGVNNSVVPVVTAPLSGVVGSGLP 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US SN 07/956,700 FILING DATE: 02-0CT-1992 PRIOR APPLICATION DATA: US PCT/US93/09340 FILING DATE: 30-SEP-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US SN 08/422,560 FILING DATE: 14-APR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE,DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08611107
Patent No. 5801233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6:
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PRIOR APPLICATION NUMBER: 0
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US-08-611-107-6
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Best Local Similarity
Matches 216; Conserv
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CITY: Houston
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APPLICATION NUMBER:
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                                                                                                                12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAY 71
                                                                                                                                     Gaps
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                                                            DB 2; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08468793
Patent No. 6177267
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: GORDIAN, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
                                                        17.9%; Score 1036.5; DB 2; Length 48.4%; Pred. No. 1e-73; Live 73; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793
FILING DATE: 06-JUN-1995
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SYSTEM: PC-DOS/MS-DOS/ASCII
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                                                                                      Conservative
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CORRESPONDENCE ADDRESS:
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                                                                        Similarity
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STRANDEDNESS
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US-08-422-560A-6
                                                                                    Matches 216;
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191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.9%; Score 1036.5;
                                                                                                                    RECISTRATION NUMBER: 33,238
RECISTRATION NUMBER: 33,238
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 NIGFLRALLREEDFTSKRIATGFIAD 456
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PCT/US93/09340
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Patent No. 5801233
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APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: NUCLEIC ACI
TITLE OF INVENTION: ACETYL-COA
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           TELEFAX: (/LZ,
TELEFAX: 79-0924
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
"VPF: amino acid
"VPF: amino acids
"VPF: single
                      FILING DATE: 30-SEP-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.48;
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Matches 216; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 430
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                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    PRIOR PAPELICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422,560
FILING DATE: 14-APR-1995
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                           APPLICATION NUMBER: US/08/611,107
FILING DATE: Concurrently Herewith
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United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kitchell, Barbara S. REGISTRATION NUMBER: 33,92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                         800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209;
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Best Local 3
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72 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 IAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVT 310
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                                                                                                                        TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND TITLE OF INVENTION: METHODS FOR USE NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS: ADDRESSE: Annold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.4%; Score 1004.5; DB 2; Length
47.1%; Pred. No. 3.5e-71;
tive 72; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/422,560A FILLING DATE: 14-APR-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/956,700 FILING DATE: 02-OCT-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 8, Application US/08422560A Patent No. 5910626
                                              GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37,259
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TELEPHONE: 512-418-3000
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
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ZIP: 77210-4433
COMPUTER READABLE FORM:
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GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
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LENGTH: 453
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359 YLPPGGPGVRVDSHVYTDYEIPPYYDSLIGKLIVWGATREEAIARMQRALRECAITGLPT 418
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                                                                                                                                                                                                                                  TITLE OF INVENTION: ACETYL-COA CARBOXXLASE COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.08/422,560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.4%; Score 1004.5; DB 3; 47.1%; Pred. No. 3.5e-71; tive 72; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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                                                               419 TLSFHOLMLOMPEFLRGELYTNFV 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US93/09340 FILING DATE: 30-SEP-1993
                                 431 NIGFLRALLREEDFTSKRIATGFI 454
                                                                                                                                                                                                                                                                                                        Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                               Sequence 8, Application US/08468793 Patent No. 6177267
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NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                APPLICANT: Haselkorn, Robert APPLICANT: Gornicki, Piotr
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TELEFAX: (713) 789-2679
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APPLICATION NUMBER: US SI
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amino acid
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Best Local Similarity 47.1%
Matches 209; Conservative
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                                                                                                                                                                                                                                                                                                                      P.O. Box 4433
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MOLECULE TYPE: protein
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                                                                                                                                                                                  GENERAL INFORMATION:
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TELEX: 7
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191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250
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                                                                                                                                                                                                                                                                                                                                                EEVIEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 370
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122 ETMQRVGVPTIPGSDGLLTDVDSAAKVAAEIGYPVMIKATAGGGGRGMRLVREPADLEKL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 FLAAQGEAEAAFGNPGLYLEKFIDRPRHVEQILADAYGNVVHLGERDCSIQRRHQKLLE 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 EAPSPALSADLRQKMGDAAVKVAQAIGYIGAGTVEFLVDATGNFYFMEMNTRIQVEHPVT 301
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                                                                                                                 182 FLAAQGEAEAAFGNPGLYLEKFIDRPRHVEFQILADAYGNVYHLGERDCSIQRRHQKLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GORNICKI, FIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE OF ENVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD.338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR PLILING DATE: 1995-06-07
PRIOR FILING DATE: 1992-10-02
SOFTWARE: PALEGATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-22
SOFTWARE: PALEGATION VOX: 2.1
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; Mismatches 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 121, Application US/09433043B; Patent No. 6399342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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311 EEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 370		371 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAI 430		431 NIGFLRALLREEDFTSKRIATGFI 454	419 TLSFHQLMLQMPEFLRGELTTNFV 442
311	302	371	359	431	419
Qγ	qa	Qy	qq	QY	q ₀

Search completed: September 24, 2003, 15:43:57 Job time: 21.8668 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 24, 2003, 15:41:22; Search time 36.2299 Seconds (without alignments) 4760.992 Million cell updates/sec Run on:

US-09-974-973A-19 5788

1 MSTHTSSTLPAFKKILVANR.....RVVVPAATKVEGGDLIVVVS 1140 Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

566894 seqs, 151307093 residues Searched:

Total number of hits satisfying chosen parameters:

566894

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 19 Appl	Sequence 4265 an	Segmence 2 annul	Sequence 2. Appli			Sequence 10806	Sequence 12361. A	Sequence 6. Appli	Sequence 8. Appli	Sequence 5215. An	Segmence 13885 A	Section of 11160 A	Spanonce 13617 a	Sequence 14226, A
SUMMARIES	e.	US-09-974-973-19	US-09-738-626-4265	US-10-045-072-2	US-09-974-973-2	US-09-974-973-4	US-09-815-242-5468	US-09-815-242-10806	US-09-815-242-12361	US-09-767-479-6	US-09-767-479-8	US-09-815-242-5215	US-09-815-242-13885	US-09-815-242-11160	US-09-815-242-13617	US-10-156-761-14226
	DB	10	10	15	10	10	σ	σ	σ	6	σ	6	6	σ	6	15
	Match Length DB	1140	1140	1140	1157	1157	1147	1142	1073	447	453	471	449	448	455	1171
% Query	Match	100.0	100.0	100.0	99.5	99.5	43.0	42.7	39.7	17.9	17.4	16,9	16.5	16.3	16.3	16.3
	Score	5788	5788	5788	5759	5759	2488	2472.5	2299	1036.5	1004.5	976.5	957	946	942.5	942
Result	No.	Н	7	3	4	Ŋ	9	7	80	6	10	11	12	13	14	15

Sequence 13364. A	Sequence 10330. A	Sequence 12063. A	Sequence 11321, A	Sequence 10924, A	Sequence 10874. A	Sequence 17, Appl	Sequence 4963, Ap	Sequence 2, Appli		Sequence 25, Appl	Sequence 11558, A	Sequence 26, Appl	Sequence 12811, A	Sequence 6940. Ap	Sequence 5418, Ap	Sequence 12562, A	Sequence 5806, Ap	Sequence 13127, A	114	Sequence 28, Appl	Sequence 12939, A	Sequence 10, Appl	Seguence 8, Appli	'n	Sequence 5, Appli	031	24	ò	Sequence 240, App
9 US-09-815-242-13364	US-09-815-	7	US-09-815-242	US-09-815-242-	5 US-10-156-76	5 US-10-16	42	5 US-10-224-539A	5 US-10-2;	2 US-10-045-612A	9 US-09-815-242-11558	US-10-045-612A-2		US-09-738-626	US-09-815-242-541	US-09-815-242	9 US-09-815-242-5806	US-09-815-242	US-10-156-761-1			US-09-767-479	a	5 US-10-083-35	US-10-224	-60-SD	-09-895-913A-	US-10-210-115-	9 US-09-205-658-240
455	449	449	458	456	590	725	443	725	725	290	455	590	700	591	446	453	448	451	919	464	358	2257	2257	483	262	158	163	1073	124
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16	17	18	19	20	21	22	23	24	25	. 26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT US-09-9 Seque Pacel GENEF APPI FILLI FILLI FILLI FULC CURA CURA CURA CURA CURA CURA CURA CUR	RESULT 1 US-09-974-973-19 TO Sequence 19, Application US/09974973 Sequence 19, Application US/09974973 Patent No. US2002017202A1 GENERAL INFORMATION: APPLICANT: Hanke, Paul D. TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter: FILE REFERENCE: 1533.1230001/MAC/RGM CURRENT APPLICATION NUMBER: US/09/974,973 CURRENT FILING DATE: 2000-10-13 PRIOR PELING DATE: 2000-10-13 NUMBER OF SEQ ID NOS: 19 SEQ ID NO 19 LENGTH: 1140 TYPE: PATENTH: US OF
Qu Be Ma	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVR 60
QY	61 IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV 120
ÃÕ đã	121 IDLIGDKSRAVTAAKKAGLPVLAESTPSKNIDBIVKSAEGQTYPIFVKAVAGGGGRGMRF 180
Oy	181 VASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCS 240

2

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059

YOKOI, HARUHIKO TATEISHI, NAOKO SENOH, AKIHIRO

APPLICANT: APPLICANT: APPLICANT:

IKEDA, MASATO

APPLICANT:

Corynebacterium glutamicum

SOFTWARE: PatentIn ver. 3.0

1140

LENGIH:

TYPE: PRT

ORGANISM:

SEQ ID NO 4265

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GVVTVIVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIVVVS 1140
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                                                          PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG 360
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                    LORRHOKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN 300
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                                                                                                                                       AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLADV
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                          DB 10; Length 1140;
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                        100.0%; Score 5788;
100.0%; Pred. No. 0;
Live 0; Mismatches
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US-09-738-626-4265
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Matches 1140;
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Sequence 4265, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:

US-09-738-626-4265

MIZOGUCHI, HIROSHI ANDO, SEIKO HAYASHI, MIKIRO OCHIAI, KEIKO

APPLICANT: NKKAGANA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI APPLICANT: ANDO, SBIKO APPLICANT: HAYASHI, MIKIRO APPLICANT: OCHIAI, KEIKO

Db 181 VASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCS 240 Qy 241 LQRRHQKVVEIAPAQHLDPELRDRICADAVKPCRSIGYQGAGTVEFIVDEKCNHVFIEMN 300	Db 241 LQRRHQKVVEIAPAQHLDPELBRICADAVKFCRSIGYQGAGTVEELVDEKGNHVFIEMN 300	OY 301 PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGITQDKIKTHGAALQCRITTEDPNNG 360 	4 4	Qy 421 AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHILQAPPADDEQGRILDYLADY 480 DD 421 AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHILQAPPADDEQGRILDYLADY 480	QY 481 TVNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAVIDTT 540	QY 541 FRDAHGSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDE 600 11111111111111111111111111111111111	OY 601 IREAMPNVNIQMILKGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPA 660	OY 661 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEBIVKSGAHILAIKDMAGLLR 720 1	OY 721 PAAVTKLYTALRREFDLPVHYHTHDIAGGQLATYFAAAQAGADAVDGASAPLSGTISQPS 780 	OY 781 LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840 111111111111111111111111111111111111	QY 841 SNLEAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGVDPADF 900 11 </th <th>QY 901 AADPOKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEGAHLDA 960 </th> <th>QY 961 DDSKERRNSLARILEPKPTEEFLEHRRREGNTSALDDREFFYGLVEGRETLIRLPDVRTF 1020 </th> <th>QY 1021 LLVRLDALSEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1080 </th> <th>Qy 1081 GVVTVTVABGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIVVVS 1140 Db 1081 GVVTVTVABGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIVVVS 1140</th> <th>RESULT 4 US-09-974-973-2 ; Sequence 2, Application US/09974973</th> <th><pre>// Patent No. US20020177202A1 // GENERAL INFORMATION: // APPLICANT: Hanke, Paul D. // TITLE OF INVENTION: Feedback-Resistant Permyate Carboxvlase Gene from Corvnebacter</pre></th> <th></th>	QY 901 AADPOKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTEVPEEGAHLDA 960	QY 961 DDSKERRNSLARILEPKPTEEFLEHRRREGNTSALDDREFFYGLVEGRETLIRLPDVRTF 1020 	QY 1021 LLVRLDALSEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1080 	Qy 1081 GVVTVTVABGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIVVVS 1140 Db 1081 GVVTVTVABGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIVVVS 1140	RESULT 4 US-09-974-973-2 ; Sequence 2, Application US/09974973	<pre>// Patent No. US20020177202A1 // GENERAL INFORMATION: // APPLICANT: Hanke, Paul D. // TITLE OF INVENTION: Feedback-Resistant Permyate Carboxvlase Gene from Corvnebacter</pre>	
Db 661 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMABEIVKSGAHILAIKDMAGLIR 720 Qy 721 PAAVTKLVTALRREFDLPVHVHTHDTAGGQLATVFAAAQAGADAVDGASAPLSGTTSQPS 780	721 PAATKLVTALRREFDLPVHVHTHDTAGGGLATYFAAAQAGADAVDGASAPLSGTTSQPS 78	VI /01 LSALVAAKAHIKKUTGLSLEAVSDLEPYWEAVRGLYLPFESGTEGPTGRVYRHEIPGGGL 840 	QY 841 SNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAGYDPADF 900 [1]	QY 901 AADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEGKAPLTBVPEEEGAHLDA 960 	QY 961 DDSKERRNSLNRLLFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLEDVRTP 1020 	OY 1021 LLVRLDAISEPDDKGMRNVVANVNGQIRPMRVRDRSVESVTATAEKADSSNKGHVAAPFA 1080 	QY 1081 GVVTVTVAEGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAATKVEGDLIVVVS 1140 	RESULT 3 US-10-045-072-2 ; Sequence 2, Application US/10045072	що	<pre>; APPLICANT: Willis, Laura B. ; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum ; FILE REFERENCE: 1533.0790002 ; CURRENT APPLICATION NUMBER: US/10/045,072</pre>	CURRENT FILING DATE: 2002-01-15 PRIOR PAPLICATION NUMBER: US 09/677,575 PRIOR FILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: US 09/220,081	co ₂	; LENGTH: 1140 ; TYPE: PRT ; ORCANISM: COFYnebacterium glutamicum US-10-045-072-2	Query Match 100.0%; Score 5788; DB 15; Length 1140; Best Local Similarity 100.0%; Pred. No. 0; Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AIYPREDRGSFHRSFASEAVR 60	Oy 61 IGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEV 120 	QY 121 LDLTGDKSRAVTAAKKAGLEVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRF 180 	Qy 181 VASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHTEVQILGDHTGEVVHLYERDGS 240

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                                                                                        Score 5759;
Pred. No. 0;
 60/239,913
                                                            ORGANISM: Corynebacterium glutamicum
PRIOR APPLICATION NUMBER: US 6C
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
                                                                                          99.5%;
99.4%;
                                                                                                           Conservative
                                                                                                 Local Similarity
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Matches 1133;
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                                   SEQ ID NO 2
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Sequence 4, Application US/09974973
Patent No. US2002017202A1
GENERAL INFORMATION:
APPLICANT: Hanke, Paul D.
TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter:
FILE REPRESENCE: 1333123000L/MAC/RGM
CURRENT APPLICATION NUMBER: US/09/9744,973
CURRENT FILING DATE: 2001-10-21
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Pred. No. 0;
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PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 19
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99.4%;
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LENGTH: 1157
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                                                            FRDAHQSLLATRVRSFALKPAABAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDE
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE ON TWENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-23
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Patent No. US20020061569A1
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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                                                                                                                                                                                                                   Length 1147;
                                                                                                                                                                                                            coh 43.0%; Score 2488; DB 9; Length 1 11 Similarity 45.2%; Pred. No. 1.5e-190; 527; Conservative 192; Mismatches 384; Indels
                                             PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001.02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5468
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                         ; ORGANISM: Staphylococcus aureus US-09-815-242-5468
                                                                                                                              LENGTH: 1147
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ORGANISM:
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QY 827 TGRVYRHEIPGGOLSNLRAQATALGLADRPELIEDNYAAVNEMLGRPTKVTPSSKVVGDL 886 : : :		OY 947 LTEVPEEEQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRRGNTSAL 995	QY 996 DDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISBEDDKGMRNVVANVNGQIRFMRVRDR 1055	QY 1056 SVESVTATAEKADSSNKGHVAAPPAGVVT-VTVAEGDEVKAGDAVAIIEAMKMEATITAS 1114	Oy 1115 VDGKIDRVVVPAATKVEGGDLIVVV 1139	RESULT 7 US-09-815-242-10806 ; Sequence 10806, Application US/09815242	<pre>; Patent No. US20020061569A1 ; GENERAL INFORMATION: ; APPLICANT: Haselbeck, Robert ; APPLICANT: Oblsen, Kari L.</pre>	; APPLICANT: Zyskind, Judith W. ; APPLICANT: Wall, Daniel ; APPLICANT: Trawick, John D. ; APPLICANT: Carr, Grant J.	; APPLICANT: Yamamoto, Robert T.; APPLICANT: Xu, H. Howard; TILLE OF INVENTION: Identification of Essential Genes in; TITLE OF INVENTION: Prokarvotes	; FILE REFERENCE: ELITRA.011A, ; CURRENT APPLICATION NUMBER: US/09/815,242 ; CURRENT FILING DATE: 2001-03-21 ; PRIOR APPLICATION NUMBER: 60/191.078	FRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 FRIOR PILING DATE: 2000-05-23 FRIOR APPLICATION NUMBER: 60/207, 727	PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/242,578 PRIOR PILING DATE: 2000-10-23 PRIOR APPLICATION NUMBER: 60/253.625	; PRIOR FILING DATE: 2000-11-27 ; PRIOR APPLICATION NUMBER: 60/257,931 ; PRIOR FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: 60/269.308	; PRIOR FILING DATE: 2001-02-16 ; NUMBER OF SEQ ID NOS: 14110 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 10806	; LENGTH: 1142 ; TYPE: PRT ; ORGANISM: Enterococcus faecalis US-09-815-242-10806	Query Match 42.7%; Score 2472.5; DB 9; Length 1142; Best Local Similarity 45.8%; Pred. No. 2.7e-189; Matches 532; Conservative 185; Mismatches 386; Indels 59. Gans 17.	ILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL 7:	

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961 DDSKE------RRNSINRILFPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRE 1009
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                                                                                                       404 FPNVEKRPKPDYELASIPTVSSSKIASFSGTKQILDEVGPKGVAEWVKKQDDVLLTDTTF 463
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                                                                        -RGSRDRLKQLGPAAFARDLREQDALAVTDTTF
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                                                                                                                                              542 RDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDEL
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          359 KNKKFTSGDYTTKFIEETPELFDIQPSLDRGTKTLEYIGNVTIN-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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ADDRESSEE: Arnold, White & Durkee
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Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA
METHODS OF
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STATE: Texas
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                                                                                                                                                                                                      APPLICANT: 2yesind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Carr, Grant D. APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Profaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.7%; Score 2299; DB 9;
Best Local Similarity 44.8%; Pred. No. 2.1e-175;
Matches 489; Conservative 179; Mismatches 361;
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRALOLLS
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: 60/207, 727
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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1118 TVDHIXVEEGEAISSGDLLLEV 1139
                                                                                                               Sequence 12361, Application US/09815242 Patent No. US20020061569A1
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PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                       APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                    GENERAL INFORMATION:
                                                                                               -09-815-242-12361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 TAAKKAGLPVLAESTPSKNID-EIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
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SOFTWARE: Patentin Release #1.0, Version #1.30
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             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/767,479
FILING DATE: 22-Jan-2001
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,793
FILING DATE: CUNKNOWN>
FILING DATE: 02-OCT-1992
                                                                                                                                                                                                                                                            NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US93/09340
FILING DATE: 30-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-767-479-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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Best Local Similarity 48.49
Matches 216; Conservative
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191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250
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                  TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.4%; Score 1004.5; DB 47.1%; Pred. No. 5.1e-72; ive 72; Mismatches 158
                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,793
FILING DATE: «Unknown>
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/09340
                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/767,479
FILING DATE: 22-Jan-2001
CLASSIFICATION: UNKnown
                                                                                                                                                                    COUNTRY: United States of America 21P: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-09-767-479-8
                                      METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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LENGTH: 453 amino acids
Gornicki, Piotr
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                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                      NUMBER OF SEQUENCES:
                                                                                                                                CITY: Houston
                                                                                                                                                    STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Sequence 8, Application US/09767479 Patent No. US20010036654A1 GENERAL INFORMATION:

US-09-767-479-8

APPLICANT: Haselkorn, Robert

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US-09-815-242-13885
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              308
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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371 YRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 430
                 73 DIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AAKKAGLPVLAESTPS----KNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRFVASPDEL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SMIAAGVP----CTPGTEGNVADLAEALREAERIGYPVMLKATSGGGGRGIRRCNSREEL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 RKLATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 VVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEH 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 KKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIGTEGSPVKAYL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                               APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamorto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%; Score 976.5; DB 9;
45.7%; Pred. No. 9.7e-70;
tive 73; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                      431 NIGFLRALLREEDFTSKRIATGFI 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-110-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                   Sequence 5215, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Les 208; Conservative
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Matches
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368 ITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSG 427
                                                                                                                                       TVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGT 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 AKKAGLPVLAESTPSKNIDEIVKSAEGQT--YPIFVKAVAGGGGRGMRFVÄSPDELRKLA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMIKABAKAAFSNDMYYMEKYLENPRHIEIQVLADGQGNAIYLAERDCSMQRRHQKVVEE 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yannoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                        428 VATNIGFLRALLREEDFTSKRIATGFIADHPHLLQ 462
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13885, Application US/09815242
Patent No. US20020061569A1
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 206; Conserva
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US-09-815-242-13885
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191 ATEASREAEAAFGDGAVYVERAVINPQHIEVQILGDHTGEVVHLYERDCSLQRRHQKVVE 250
                               242 EAPAPGITEEVRRDIGSRCANA---CVEIGYRGAGTFEFLY-ENGEFYFIEMNTRIQVEH 297
                                                                                                                                                                                                           368 ITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 LDIDEIIGAAKKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAV 131
                                                                                             251 IAPAQHLDPELRDRI----CADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEH
                                                                                                                                                                                 308 IVTEEVTEVDLVKAQMRLAAGATLKELGLIQDKIKTHGAALQCRITTEDPNNGFRPDTGT
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DENALTYCES

TITLE OF INVENTION: ELITRA. 011A
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21/1078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 630
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-60/253, 630
PRIOR PRILING DATE: 2000-12-16
PRIOR PRILING DATE: 2001-02-16
PRIOR PRILING DATE: 2001-02-16
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Pred. No. 5e-67;
5; Mismatches 160;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020061569A1
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46.0%; Pre-
tive 75;
                                                                                                                                                                                                                                                                                                                                                          428 VATNIGFLRALLREEDF 444
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT:
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Best Local
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                                                                                                                                                                      372 RSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATN 431
                         312 EVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAY 371
                                                                                                        358 HAPGGFGVRWESHIYAGYTVPPYYDSMIGKLICYGENRDVAIARMKNALQELIIDGIKTN 417
252 APAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMNPRIQVEHTVŢE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AAKKAGLPVL--AESTPSKNIDEIVKSAEGOTYPIFVKAVAGGGGRGMRFVASPDELRKL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.3%; Score 946; DB 9; Length 448; 47.6%; Pred. No. 2.5e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PROKALYOUS
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
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2yskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yammoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                      418 IDLOTRIMNDEHF 430
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                                                                                                                                                                                                                                                             432 IGFLRALLREEDF 444
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Best Local Similarity 47.65
Matches 208; Conservative
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TAAKKAGLPVLAESTPS-KNIDEIVKSAEGG	PESULT 15 PESULT 15 PESULT 15 Sequence 14226, Application US/10156761. PUDICATION US20030119018A1 GENERAL INFORMATION OF US20030119018A1 APPLICANT: KEDA, HARUO APPLICANT: IKEDA, HARUO APPLICANT: SHIBA, TADAYOSHI APPLICANT: SALANI, YOSHIYUKI APPLICANT: SALANI, YOSHIYUKI APPLICANT: SALANI, YOSHIYUKI APPLICANT: SALASINA APPLICANT: SALOSHO OF POLONO	tch 16.3%; Score 942; DB 15; Length 1171; al Similarity 28.1%; Pred. No. 2.66-65; 368; Conservative 145; Mismatches 471; Indels 326; Gaps 44; 12 FKKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRICHEGSPVK-A 70
	RESULT 15 US-10-156 Sequence Publicat GENERAL APPLICY	Ouery Match Best Local S Matches 368 QY 12 Db 61 QY 131 QY 131 Db 121 QY 191 QY 191 QY QY 191 QY 191 QY 191 QY 191

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310 TEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTIT 369
                                                                                       301 TEELYGVDLVAWMLRLAGG----DADVVRDPGPPRGHAVEARVYAEDPSREHRPSAGLLT 356
                                                                                                                             370 AYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1053 R------DRSVESVIATAEKADSSNKGHVAAPFAGVVT-----VTVAEG 1090
                                                                                                                                                         415 TNLGLVRAALADHGLRTATHTTATLAKITDPTPRVEVVAAGTLTTVQDWPGRTGYWQVGV 474
                                                                                                                                                                                                                                                                                   461 LQAPPADD------EQGR-----EQGR-------ILDYLADVTVNKPHG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             994 ALDDREFFYGLVEGRETLIRL-PDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIRPMRV 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1002 --FDRIKWYAV--GPDELLDLRADIASGRFVPRVEEGEFSLAGYESFLAANAGSIAAFRA 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1058 ROGAAFAAERDAWEAAGEFARAEAATAPEAPPAEVIVPVGGALVEAEFAASVWQLNVGPG 1117
                                                                                                                                                                                                                                                                                                                                                               488 VRPKDVAAPIDKL------ARDLFLPRGSRDRLKQLGPAAF------ARDLR 529
                                                                                                                                                                                                                                                                                                                                                                                         530 EQDALAVIDITFRDA----HQSLLATRVRSFALKPAAEAVAKLIPELLSVEAWGGATYD 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595 IGDVLHGGSVIDRGAPVPAGDRPVFAIEWHVGALEGPHAAPEFFIED--DIRDFYAAGWK 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 V-----AMRELFEDP-WDRLDELREAMPNVNIQMLLRGRNTVGYT---PY---PDS-- 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        653 VHFNSARTGVRLVGPKPRWARSDGGEAGLHPSNIHDTPYSVGAVDYTGDMPVLLGPDGPS 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                713 IGGFVCPATVATAERW---- 742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    743 ------PLAEDGSTRPALVDGGVLARDGDVTYRRSGDDNLLVEFGPMQLD 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737 LPVHVHTHDTAGGQLATYFAAAQAGADAV-------DGASAPLSGTTSQPSLS 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    787 LALRMRVH------ALMEAVAEAGLDGVTDLTPGIRSLQIRTDPRRLPLR-----ELL 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        783 AIVAAFAHTRRDIGLSLEAVSDLEPYWEAV---RGLYLPFESGIPGPIGRVYRHEIPGGQ 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   840 LSNLRAQA-----TALGLADRFELIEDNYAAVNE----MLGRPTKVTPSSKVVGDLAL 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             889 HLVGAGVDPADFAADPQ-----KYDIPDSVIAFLRGELGNP------PGGWPEPLR 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924 ---GA---PVATPLDPRHRLVTTKYNPARTWTAENSVGIGGAYLCVYGMEGPGGYQFVGR 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       934 TRALEGRSEGKAPLIEVPEEEQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRRFGNIS 993
                                                                                                                                                                                                                                                                                                                         475 PPCGPMDDRSFRLGNRALGNEEGAPGLECTLRGPALRFTHATTVCVTGAPAPVTVDGTPV
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Search completed: September 24, 2003, 15;53:13

Job time : 42,2299 secs